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4, 2005, 11:54:40 , Search time 147.676 Seconds (without alignments) 861.643 Million cell updates/sec
                                                                                                                                                                                                                         1 MAQHHLWILLLCLQTWPEAA......KASTQDSKPPGTSSYEIVIX 329
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1696
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003as:*geneseqp2003bs:*

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

A_Geneseq_16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:*

Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

STIMMEDIES

No.	,	Query	٠	1		
	Score	Match	Match Length	8	ID	Description
-	1695	99.9	328	Ŋ	AAB47878	Aab47878 SCZ/CD84.
7	1695	99.9	328	Ŋ	AAE26238	Aae26238 Human CD8
m	1695	99.9	328	œ	ADL82907	
4	1695	66.66	328	œ	AD005708	Ado05708 Human leu
2	1695	6.66	328	œ	ADQ19067	_
9	1695	99.9	328	œ	ADP23943	~
7	1695	99.9	329	~	AAW74891	-
80	1695	6.66	329	'n	ABG95343	Abg95343 Human nov
6	1695	99.9	329	9	AB034537	Region
10	1695	99.9	329	7	ADI23198	Adi23198 Novel hum
11	1695	99.9	329	8	ADH74200	Adh74200 Human sec
12	411	24.2	79	7	AAY12524	Aay12524 Human 5'
13	382.5	22.6	551	ß	ABG96270	Abg96270 Human imm
	382.5	22.6	565	œ	ADK98560	_
	382.5	22.6	610	S	AAU74425	Human
	378.5	22.3	526	80	ADL57243	Human
	378.5	22.3	526	æ	ADL57105	Adl57105 Human NOV
	378.5	22.3	615	æ	ADL57103	Ad157103 Human NOV
	374	22.1	654	Φ	AD063782	Ado63782 Human Ly-
20	374	22.1	654	80	ADO78174	Human
21	373	22.0	289	4	AAE12078	Aae12078 Dendritic
22	373	22.0	289	Ŋ	AAE26243	Aae26243 Human CD2
23	373	22.0	289	Ŋ	ABP65110	Abp65110 Hypoxia-i
24	373	22.0	289	7	ABW01823	Human
25	370	21.8	289	ഹ	AAE26250	Aae26250 Human CD2

Human (Aae26252 Human CD2	Abw01830 Human CD2	Abw01831 Human CD2	Human (Aae26253 Human CD2	Human	_	Aay66701 Membrane-	Ξ.	Aay44609 Human myo	Human	Aab87548 Human PRO	APEX-1	Aab65224 Human PRO	Abg95873 Human sec	Abu58495 Human PRO	Abu88043 Novel hum	Abu84358 Human sec	Abr66232 Human sec	
AAE26251	AAE26252	ABW01830	ABW01831	ABW01832	AAE26253	ABW01833	AAU09868	AAY66701	AAY70431	AAY44609	AAU29119	AAB87548	AAB47321	AAB65224	ABG95873	ABU58495	ABU88043	ABU84358	ABR66232	
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289	289	289	289	289	289	289	346	335	335	335	335	335	335	335	335	335	335	335	335	
8.1	1.8	8.1	8.1	8.1	1.8	21.8	21.4	1.4	1.4	1.4	1.4	1.4	21.4	1.4	1.4	4.4	1.4	4.1	1.4	
7	~	'n	N	2	7	7	7	2	7	2	~	~	~	N	~	~	N	N	~	
370	370	370	370	370	369	369	363.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	
56	27	28	29	30	31	32	33	34	35	36	37	38	68	40	41	42	4.3	44	45	

ALIGNMENTS

Diagnosing susceptibility to schizophrenia (SC2) in a patient, by determining presence or absence of an allele of a linked polymorphic marker present on chromosome 1g22, were the marker is linked to a variant form of the SCZ gene. SCZ; CD84; platelet; monocyte; circulating B cell; schizophrenia; allele; polymorphic marker; chromosome 1q22. (RUTF) UNIV RUTGERS STATE NEW JERSEY. Š AAB47878 standard; protein; 328 23-APR-2001; 2001WO-US013040. 21-APR-2000; 2000US-0198873P. Brzustowicz LM, Bassett AS; (first entry) WPI; 2002-171605/22. N-PSDB; AAI72383. WO200202054-A2. Homo sapiens 10-JAN-2002. 02-MAY-2002 AAB47878; SCZ/CD84. RESULT 1 AAB47878

Example 6; Page 70; 82pp; English.

This sequence is encoded by the SCZ gene which was isolated using the method of the invention. The SCZ gene has been previously identified as CD84, GenBank Accession No: NM 003874. CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. This protein may be involved in the processes by which the brain responds to biological stimuli. Therefore they may provide targets for therapeutic intervention in the treatment of schizophrenia. The SCZ sequence may be used in a new method of diagnosing susceptibility to schizophrenia in a patient. The method comprises determining the presence or absence of an allele of a linked polymorphic marker in the DNA of the patient. The polymorphic marker is present in chromosome 1q22 and is linked to a gene (SCZ) having

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                                                                                                                                                                                 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                                                                                                    1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                         MAQHHLMILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
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                                                                                                                                                                                                                                            TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
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                                                            Length 328;
a variant form associated with a phenotype of schizophrenia
                                                                                       Indels
                                                       99.9%; Score 1695; DB 5;
100.0%; Pred. No. 8e-138;
ive 0; Mismatches 0;
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                                                            100.0%; FI
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                                                                                         Conservative
                                                                    Local Similarity
hes 328; Conserv
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                           Sequence 328 AA;
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(MILL-) MILLENNIUM PHARM INC.

Fraser CC;

WPI; 2002-620680/67. N-PSDB; AAD43563.

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The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains and SIAMA associated protein (SAP) motifs. CD2000 DNA and protein is cuseful for treating disorder such as immune proliferative disorders, useful for treating disorder such as immune proliferative disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g. arthritis, multiple sclerosis, Grave's disease, and Hashimoto's clesase). T cell disorder (e.g. acquired immune deficiency syndrome (AIDS)), inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), inflammatory disorders (e.g. rheumatorid arthritis and costeoarthritis), alpoptotic disorders (e.g. rheumatory disorders) septic shock, colitis), apoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cyctoxic disorders, septic shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive comedicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and phramacogenomics), and in methods of treatment (e.g. thereful on the invention
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Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
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Matches 328; Conservative
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The invention relates to treating a subject having a condition that

benefits from modulating the balance of regulatory T cell function

crelative to effector T cell function, or vice versa, in a subject. The

method involves administering an agent that modulates the expression or

activity of a molecule selected from PTGER2 and TGFbetal, or Jagged-1,

GRP-32, CD83, CD84, CD89, serotonin R, BYS5, serotonin R2C, GRR63,

Chistamine R-H4, GPR58, ED9-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-

CC are useful for diagnosing, preventing or treatment occurs. The methods

are useful for diagnosing, preventing or treatment occurs. The methods

call response to antigens associated with the condition, such as in an

allergic response, an autoimmune disorder, a viral infection, a microbial

cinfection, a parasitic infection or a tumour. The present sequence

represents a human leukocyte differentiation CD84 antigen, preferentially

expressed in regulatory T cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating a condition that benefits from modulating regulatory or effector T cell function comprises administering an agent that modulates the expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbeta1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 120
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                                                                                                                                                                                      T cell; antiallergic; immunosuppressive; virucide; antibacterial; antiparasitic; cytostatic; gene therapy; human; CD83; leukocyte differentiation antigen.
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100.0%; Pred. No. 8e-138;
ive 0; Mismatches (
                                                                                                                                                   Human leukocyte differentiation antigen CD84.
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                     ADO05708 standard; protein; 328
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09-OCT-2002; 2002US-0417103P.
09-OCT-2002; 2002US-0417243P.
18-OCT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0424777P.
08-NOV-2002; 2002US-0424881P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TOLE-) TOLERRY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jagged-1 or GPR-32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Szymanska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADO05707.
GENBANK; 6650105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 328 AA;
                                                                                                                                                                                                                                                                                                                                    WO2004032867-A2.
                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                        15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                22-APR-2004.
                                                              ADO05708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
AD005708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polygaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA confinemia of infancy, Burkit's lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumacoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO proteins are also useful for preparing a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                     New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondyllitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAQHHLMILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKRYNLOIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEBKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSVFLFRLFKREDDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                                                                                                                                                                                                                                                     Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.9%; Score 1695; DB 8; Length 328; 100.0%; Pred. No. 8e-138;
                                                                                                                                                                                                                                                                     Schoenfeld JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                     Fong S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Fig 109; 695pp; English
                                                                                                                                                                                                                                                                       Dennis K,
                                                                                                                                     15-SEP-2003; 2003WO-US029097
                                                                                                                                                                               16-SEP-2002; 2002US-0411392P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 328; Conservative
                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                         WPI; 2004-329389/30.
                                                                                                                                                                                                                                                                       Clark H,
                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADL82906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 328 AA;
                                            WO2004024097-A2.
    Homo sapiens.
                                                                                        25-MAR-2004
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic saric sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                 TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI 180
                                                                                   SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
                                                                                                                                                    soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                  FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                                                                                                                                                                                     - SEQ ID 1886.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human soft tissue sarcoma-upregulated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 1886; 210pp; English.
                                                                                                                                                                                                                        EVQFADKMGKASTQDSKPPGTSSYEIVI 328
                                                                                                                                                                                                                                                                                                                        ADQ19067 standard; protein; 328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-2003; 2003WO-US038193
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                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-441208/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinfulammatory, antiarthritic, antithemutic, immunosuppressive, osteopathic, autidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatorropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                          241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS
                           1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                                                                                              TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                               FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
                                                                                                                                                                                                                                                                                                                                                                             181 FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFPLLVLIL
MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Lookeren M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; SEQ ID NO 1121; 2940pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQFADKMGKASTQDSKPPGTSSYEIVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP23943 standard; protein; 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-2003; 2003WO-US034312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2002; 2002US-0423394P
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Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-419628/39.
N-PSDB; ADP23942.
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XXX ADP23943

XXX ADP23943

DT 18-N

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XXX OSEC
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Gaps

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Indels

DB 8; Length 328;

Query Match
99.9%; Score 1695; DB 8;
Best Local Similarity 100.0%; Pred. No. 8e-138;
Matches 328; Conservative 0; Mismatches 0

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970S-0047584P.
970S-0047585P.
970S-0047586P.
970S-0047587P.
970S-0047588P.
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9705-0047590P.
9705-0047592P.
9705-0047594P.
9705-0047594P.
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97US-0047598P.
97US-0047609P.
97US-0047601P.
97US-0047611P.
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97US-0048964P.
97US-0048974P.
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970S-0043569P.
970S-0043576P.
970S-0043578P.
970S-0043580P.
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970S-0056637P.
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970S-0056664P.
                                                        970S-0040161P.
970S-0040162P.
970S-0040333P.
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970S-0040331P.
970S-0043312P.
970S-0043312P.
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97US-0056632P
                 98WO-US004493
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23-MAY-1997;
                 06-MAR-1998;
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23-MAY-1997;
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    idiopathic inflammatory myopathy, Sjogren's syndrome, systemic claiopathic inflammatory myopathy, Sjogren's syndrome, systemic claiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous carbonic inflammatory demyelinating polymeuropathy, duillain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, a hepatobiliary circhosis, granulomatous hepatitis, sclerosing cholangitis, billary circhosis, granulomatous hepatitis, sclerosing cholangitis, ciflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, a nattoimmune or immune-mediated skin disease, asthma, allargic rhintis, atopic dermatitis, food disease, asthma, allargic rhintis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease, of the lung, conteumonitis, a transplantation associated disease, graft rejection or content content described by the sensitivity or content by the sensitivity or content described by the sensitivity or con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKRYNLQI YRRLGKPKI TQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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fusion protein; cancer; central nervous system; seizure; diagnosis;
neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                  Query Match 99.9%; Score 1695; DB 8; Length 328; Best Local Similarity 100.0%; Pred. No. 8e-138; Matches 328; Conservative 0; Mismatches 0; Indels 0
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11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC; Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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970S-0056862P
970S-0056814P
970S-0056817P
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970S-005691P
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N-PSDB; AAV59674.
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22-AUG-1997;
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AYVTPGDSETAPVVIVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                     TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                     TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                           181 FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
                                                                                                                                                   SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS
                                                                                             FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
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97US-0040161P.
97US-0040163P.
97US-0040334P.
97US-0040334P.
97US-0040331P.
97US-00403311P.
97US-0043311P.
97US-0043311P.
97US-0043311P.
97US-0043569P.
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9710S-0047501P.
9710S-0047502P.
9710S-0047581P.
9710S-005661P.
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97US - 0056893P.
97US - 0056904P.
97US - 0056908P.
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97US - 0056910P.
97US - 0056910P.
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97US-0057669P.
97US-0057761P.
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22-AUG-1997
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA secreted proteins, given in the specification. The protein is used in a condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, packed disorders e.g. alzheimer's disease, confections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound causumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The collure of primary tissues, to regenerate tissues and in chemotaxis. The collures or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents one of the novel human carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents one of the novel human carbohydrate specification, but was obtained in electronic format cortectly from USPTO at seqdata.uspto.gov/sequence.html?pocID=6420526B1
                                                                                                                                               , Rosen CA, Fischer CL, Soppet DP, Carter KC;
DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
M, Duan K, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                             New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 483; 129pp; English.
                    97US-0061060P.
98WO-US004493.
97US-0058785P
                                                                                                (HUMA-) HUMAN GENOME SCI INC
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N-PSDB; ABS73661.
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Moore PA, Shi Y,
12-SEP-1997;
02-OCT-1997;
06-MAR-1998;
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Bednarik D
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ö TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI 180 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300 9 61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 1 MAQHHLWILLLCLQTWPEAAGKDSBIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV FOTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 0; Gaps 5; Length 329; 0; Indels 99.9%; Score 1695; DB 5; L. 100.0%; Pred. No. 8.1e-138; ive 0; Mismatches 0; Query Match 99.9 Best Local Similarity 100. Matches 328; Conservative 121 181 241 원 셤 g 셤 8 엄 8 ઠે ò

Sequence 329 AA;

EVQFADRMGKASTQDSKPPGTSSYEIVI 328

241 301 301

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3 - MAX - 1997 | 97105 - 0047594P.
3 - MAX - 1997 | 97105 - 0047596P.
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RUBE/)
(ROSE/)
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(YUGG/)
(NIJJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CART/)
Human; secreted protein; hyperproliferative disorder; leukaemia;

Mreast cancer; wound; reproductive disorder; blood-related disorder;

Mremophilia; thrombocytopaemia; immunodeficiency; thymic hypoplasia;

Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

W viral infection; bacterial infection; fungal infection; AIDS; sepsis;

W main infection; bacterial infection; fungal infection; AIDS; sepsis;

renal disorder; kidney failure; cardiovascular disorder; cytostatic;

W angina pectoris; cerebral isobaemia; congenital heart defect;

Respiratory disorder; neurological disorder; Alzheimer's disease;

W Parkinson's disease; inflammation; Crohn's disease; vulnerary;

immunosuppressive; antibacterial; haemostatic; thrombolytic;

antiacoagulant; neuroprotective; thyromimetic; antiallergic;

antiacthmatic; virucide; fungicide; antiparkinsonian;

m antiinflammatory.
                                                                                                                Region of human secreted protein encoded by cDNA sequence #164.
                                  ABO34537 standard; protein; 329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0038621P
97US-0040163P
97US-0040334P
97US-0040334P
97US-00403312P
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97US-004563P
97US-004758P
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                                                                                       (first entry)
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07-MAR-1997;

11-APR-1997;

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        RESULT 9
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SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
                                                                    FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
               cytostatic; gene therapy; cancer; human; secreted protein.
                                                                                                                              EVQFADKMGKASTQDSKPPGTSSYEIVI 328
                                                                                                           EVQFADKMGKASTQDSKPPGTSSYEIVI 328
                                                                                                                                                                                                                                                                                           Novel human secreted protein seg id 483
                                                                                                                                                                                                         ADI23198 standard; protein; 329 AA
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97US-0040162P.
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97US-0040334P.
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23-MAY-1997;
23-MAY-1997;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the cyclospectine and interesting or patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
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                                                                                                                                                                                                                                                   Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Pred. No. 8.1e-138;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 483; 260pp; English.
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100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 328; Conservative
                                                                          HU J.
FLORENCE K A.
                                                                                                                           EBNER R.
BREWER L A.
MOORE P A.
SHI Y.
LAFLEUR D W.
                                                                                                     OLSEN H S.
FISCHER C L.
       FENG P.
YOUNG P E.
GREENE J M.
FERRIE A M.
DUAN D R.
                                                                                                                                                                                                                                                                                                                           WPI; 2003-521800/49.
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ZENG Z.
KYAW H.
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HU J.
FLORENCE K A.
OLSEN H S.
FISCHER C L.
BENER R.
BREWER L A.
MOORE P A.
SHI Y.
LAFLEUR D W.
LI Y.

(SHIY/) (LAFL/) (LIYY/) (ZENG/) KYAW/)

(HUJJ/) (FLOR/) (OLSE/) (FISC/) (EBNE/) (BREW/)

YOUNG P B. GREENE J M. FERRIE A M. DUAN D R.

(YOUN/) (GREE/)

(FERR/) (DUAN/)

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970S-0047595P
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
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22-AUG-1997;
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The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding a polypoptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer. The is the amino acid sequence of a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                  JM, Ferrie AM;
Ebner R;
19 Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
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                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer.
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                                                                                                                                                                                                                                                                                                  Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP, Bodress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Buan DR, Hu J, Plorence KA, Olsen HS, Fischer CL, Ebber Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z,
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N-PSDB; ADI22889.
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YU G. NI J. FENG P.

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human; secreted protein; cancer; haematopoietic disorder; endocrine disorder; immune system disease; inflammatory disorder.
               ADH74200 standard; protein; 329 AA
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9705-0047589P
9705-0047590P
9705-0047592P
9705-0047594P
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9705-0047599P
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97US-0040161P.
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97US-0047614P.
97US-0047615P.
                                                                                                                                                  2002US-00164861
                                                            Human secreted protein #164.
                                             25-MAR-2004 (first entry)
                                                                                                                   US2003225248-A1.
                                                                                                    Homo sapiens.
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11-APR-1997;
11-APR-1997;
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23-MAY-19
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RESULT 11
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Carter KC, Bednarik DP; Greene JM, Ferrie AM;
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Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Soppet DR,
     970S-0047618P

970S-0047618P

970S-0048944P

970S-0048974P

970S-0051926P

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970S-0056631P

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9705-0056892P
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Ni J,
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N-PSDB; ADH73891.
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22-AUG-1997;
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22-AUG-1997;
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05-SEP-1997;
12-SEP-1997;
02-OCT-1997;
06-MAR-1998;
              23-MAY-1997,
23-MAY-1997,
06-JUN-1997,
13-JUN-1997,
14-JUN-1997,
16-JUL-1997,
16-JUL-1997,
22-AUG-1997,
22-AUG-1997,
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The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPs) they encode. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoistic disorders, endocrine disorders, diseases of the immune system, inflammatory disorders and many others. Full details of disorders that may be

Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with aberrant expression and activity.

Claim 11; SEQ ID NO 483; 142pp; English.

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prevented, diagnosed and/or treated by the above methods are given in the specification. The nucleic acid molecules may be used to produce their proteins. The nucleic acid and it's complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which as antigens in the production of antibodies against the production of antibodies against the proteins and in assays to identify modulators of SP expression and activity. The anti-SP antibodies may also be used to down regulate expression and activity. The anti-SP antibodies may also be used to down regulate expression and activity. The anti-SP antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbat assay (ELISA)). The present sequence
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Sequence 329 AA;

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                                                                                 MAQHHLMILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                             1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                             61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                                                                                                                               61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                                                                                                                                                                            TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                  121 TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLOI
                                                                                                                                                                                                                                                         PQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
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                                 Gaps
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99.9%; Score 1695; DB 8; Length 329; 100.0%; Pred. No. 8.1e-138; ive 0; Mismatches 0; Indels
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Matches 328; Conservative
 Query Match
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AAY12524 standard; protein; 79 AA (first entry) Human 5' EST 22-JUN-1999 AAY12524;

secreted protein SEQ ID NO: 189 from WO 9906553

Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemocactic; chemokinetic; haemostatic; thrombolytic; antiinflammatory; tumour inhibition; antitumour.

Homo sapiens

WO9906553-A2

98WO-IB001237. 31-JUL-1998;

97US-00905051 01-AUG-1997;

(GEST) GENSET

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human secreted proteins, and encode the proteins given in AAV1250 to human secreted proteins, and encode the proteins given in AAV1251 to AAV12668, respectively. The proteins given represent the signal peptide and an N-terminal fragmen of a secreted human gene be to did sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, call proteins obtained may have cytokine activity, call proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemokactic/ chemokinetic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, antiinflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping promoter sequences can also be used for obtaining corresponding promoter directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
                                                                                                                                                                                                                                                              New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from umbilical cord, lymph ganglia, lymphocytes and
     Lacroix B;
Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 34; Page 323; 411pp; English.
Dumas Milne Edwards J,
                                                                                                   WPI; 1999-153783/13.
                                                                                                                                                                                                                                                                                                                                                                            placental tissue.
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. 0 24.2%; Score 411; DB 2; Length 79; 100.0%; Pred. No. 1e-27; tive 0; Mismatches 0; Indels Conservative Local Similarity nes 78; Conserv Query Match **datches**

Sequence 79 AA;

9 9 1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV 1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV 요 ð

78

61 AYVTPGDSETAPVVTVTH

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AYVTPGDSETAPVVTVTH 78 셤

ABG96270 standard; protein; 551 11-DEC-2002 (first entry) ABG96270; RESULT 13 ABG96270

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Human immunoglobulin superfamily protein IGSFP-8.

Immunoglobulin superfamily protein; IGSFP; cell proliferative disorder; arteriosclerosis; atherosclerosis, cirrhosis; hepatitis; paroxystal noctural haemoglobinuria; polycythaemia vera; psoriasis; primary thrombocytopenia; cancer; leukaemia; lymphoma; sarcoma; myeloma; autoimmune disorder; inflammatory disorder; lowpacher; autoimmunedficiency syndrome; AIDS; allergy; anaemia; asthma; autoimmune thyroiditis; contact dermatitis; Crohn's disease; diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout; Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoprosis; pancreatitis; Reiter's syndrome; rheumatoid arthritis; Sjogren's syndrome; uveitis; trauma; viral infection; bacterial infection; fungal infection; protozoal infection; helminthic infection; gene

Homo sapiens

WO200272794-A2

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YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated immune response associated protein (IRAP) comprising any of 35 fully defined sequences given in the specification. The polypeptide of the invention demonstrates antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian, hepatotropic, cerebroprotective, antiinflammatory, nootropic and vasotropic activities and may be useful for treating a disease or condition associated with decreased expression or overexpression of functional immune response associated proteins, while the antibody is useful for diagnosing a condition or disease associated with the Azhreimer's disease, Parkinson's disease and Crohn's disease. Furthermore, the molecules of the invention may be utilised during gene therapy procedures. The current sequence is that of a human IRAP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated immune response associated proteins (IRAP) polypeptide and polynucleotide, useful for diagnosing and/or treating disorders with aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OHHIWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA
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                                                                                                                                                                                                                                cytostatic; neuroprotective; antiparkinsonian; hepatotropic; cerebroprotective; antiinflammatory; nootropic; vasotropic; arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease; Parkinson's; Crohn's; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hafalia AJA, Richardson
awla NK, Khare R, Becha
                                                                                                                                                                                                              protein; IRAP; antiarteriosclerotic;
                                                                                                                                                              Human immune response associated protein IRAP-23 protein.
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    Elliott VS, Hafalia Amarquis JP, Chawla NK,

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                    ¥.
                    ADK98560 standard; protein; 565
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13.SEP-2002; 2002US-0410571P.
18-OCT-2002; 2002US-0419906P.
25-OCT-2002; 2002US-0421445P.
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                                                                    ADK98560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to new immunoglobulin superfamily proteins

(IGSFP). The polypeptides, polynucleotides, agonists and antagonists are

(seful for diagnosing, treating or preventing disorders associated with

aberrant expression of IGSFP, particularly cell proliferative, e.g.

arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal

concernal haemoglobiuntia, polycythaemia vera, psorissis, primary

thrombocytopenia or cancers including leukaemia, lymphoma, sarcoma or

myeloma, and autoimmune or inflammatory disorders, e.g. acquired

cmyeloma, and autoimmune or inflammatory disorders, e.g. acquired

cmyeloma, contact dermatitis, languages, gout, Graves' disease,

thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,

clomerulonephritis, Goodpasture's syndrome, gout, Graves' disease,

clomerulonephritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid

arthritis, Sjogren's syndrome, uveitis, trauma, or viral, bacterial,

fungal, parasitic, protozoal or helminthic infections They are also

cuseful in the assessment of the effects of exogenous compounds on the

expression of nucleic acid and amino acid sequences of IGSPP. The present

cmino acid sequence represents a human IGSPP protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARPKEN-----VTIMVKSYLGRLDITKWSYSLCISNLTLNDAGSYKAQINQRNFEVTTE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 KRYNLQIYRRLGKPKIT-QSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EBFTLFVYEQLOEPQVTMKSVKVSENFSCNITLMCSVKGAEKSVLYSWTPREPHASESNG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNVLOIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSILTVSRTPCDPDLPYICTAQNPVSQRSSLPVHVGQFCTDPGASRGGTTGET-VVGVLG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human immunoglobulin superfamily proteins and polynucleotides, useful for diagnosing, treating or preventing disorders with aberrant IGSFP expression, such as autoimmune, inflammatory or cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MFFLLVLILSS------VFLFR----LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPVTLPLALPACRDTEKVVWLFNTSIISKEREEAATADPLI-----KSRDPYKNRVW 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA
                                                                                                                                                                                                                                                                                           ı Y, Thangavelu K, Warren BA, Tang YT, Duggan BM;
Baughn MR, Honchell CD, Burford N, Forsythe IJ, Yang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.6%; Score 382.5; DB 5; 33.9%; Pred. No. 4.2e-24; ive 60; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 129-130; 145pp; English
                                                                                              12-MAR-2001; 2001US-0275249P.
31-AUG-2001; 2001US-0316B10P.
21-SEP-2001; 2001US-033977P.
25-OCT-2001; 2001US-0343880P.
                                                     12-MAR-2002; 2002WO-US009052
                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
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N-PSDB; ABS76363.
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Matches 101; Conserv
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Length 565; Indels

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usceptibility to a systemic autoimmune disorder. The method comprises screening for at least one mutation within the systemic lupus erreening for at least one mutation within the systemic lupus erreening for at least one mutation within the systemic lupus erreening for at least one mutation in a gene or genes with the SLE-1B loci such as a gene of genes with the SLE-1B loci such as a gene or genes with the SLE-1B loci such as a gene conding signalling lymphocyte activation molecule (SLAW), lymphocyte activation genes (SLAM), lymphocyte activation factor (USF)!, GD44. The method of the invention is useful for treating SLE and involves administering a construct somprishing a wild-type sequence encoding any one of the above mentioned genes. Gene therapy also involves the use of antisense constructs or ribozymes directed against the above mentioned genes for treating SLE. Note: The present protein sequence represents a human protein of the invention that relates to the isolation of genes within sign-lb that mediate a break in immune tolerance. This sequence is shown in the sequence listing but is not further defined in the specification
                                                                                                                   ---GEE 174
                                                                                        GNVLQIPQIPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for susceptibility to systemic autoimmune disorder by screening for a mutation within the systemic lupus erythematosus-1B loci.
                                                                                                                                                                                                            263 EPVTLPLALPACRDTEKVVWLFNTSIISKERBEAATADPLI-----KSRDPYKNRVW 314
                                                                                                                                                                                 232 MFFLLVLILSS-----VFLFR---LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence #3, related to isolation of genes within SLE-1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; systemic lupus erythematosus 1B; SLE-1B; dermatological; antiinflammatory; immunosuppressive; systemic autoimmune disorder; signalling lymphocyte activation molecule; SLAM; lymphocyte antigen 9; Ly-9; 2B4; natural killer cell receptor; CD48; CD84; LY108; CS1; DEDD; NIT1; upstream transcription factor 1; USF 1; GOLGA4; immune tolerance.
122 KRYNLQIYRRLGKPKIT-QSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new method for screening for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morel L;
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21-SEP-2000; 2000US-0234457P.
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YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121
                                                                                                                                                            58 FARPKEN-----VTIMVKSYLGRLDITKWSYSLCISNLTLNDAGSYKAQINQRNFEVTTE 112
                                                                                                                                                                                                             KRYNLQIYRRLGKPKIT-QSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEE 174
                                                                                                                                                                                                                               GNVLQIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLA 231
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                                                                                                                                                                                                                                                                                                                                                 232 MFFLLVLILSS-----VFLFR----LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
                                                                                                                                                                                                                                                                                                                                                                       EPVTLPLALPACRDTEKVVWLFNTSIISKERERAATADPLI-----KSRDPYKNRVW 283
                                                                    3 OHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA
                                                                                                     QTSLLFLLMGLR----ASGKDSAPTVVSGILGGSVTLPLNISVDTEIENVIWIGPKNALA
                                      Gaps
                                    37;
   Length 610;
                                    Indels
Query Match 22.6%; Score 382.5; DB 5; Best Local Similarity 33.9%; Pred. No. 4.9e-24; Matches 101; Conservative 60; Mismatches 100;
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1 MAQHHLMILLLCLQTWPEAA.......KASTQDSKPPGTSSYEIVIX, 329
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/ cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/ cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/ cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/ cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-09-949-016-6907

US-08-348-792-8

US-08-462-738-8

US-08-189-955-8

US-08-189-955-8

US-08-189-955-8

US-08-189-955-2

US-08-189-955-2

US-08-189-955-2

US-08-189-955-2

US-08-189-955-2

US-08-188-3

US-08-348-792-4

US-08-348-792-4

US-08-348-792-4

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US-08-348-792-10

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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILT REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/941,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-08

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 207012
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100.0%; Pred. No. 3.5e-166;
ive 0; Mismatches 0;
US-09-369-248A-2
US-08-348-792-12
US-08-462-738-12
US-09-199-955-12
US-09-13-999C-4353
US-09-13-99C-4353
US-09-907-794A-320
US-09-907-794A-320
US-09-905-75A-320
US-09-906-700-320
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US-09-906-708-320
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Patent No. 6812339
GENERAL INFORMATION:
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5.09-149-476-483, Application US/09149476
Sequence 483, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                     CURRENT FILING DATE: 1998-09-08
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER PILING DATE: 1998-03-06
EARLIER PELING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER PELING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R APPLICATION NUMBER: 60/047,587
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R APPLICATION NUMBER: 60/047,600

R APPLICATION NUMBER: 60/047,615

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,515

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,597

R APPLICATION NUMBER: 60/047,502

R R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,503

R APPLICATION NUMBER: 60/047,503

R APPLICATION NUMBER: 60/047,613

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R APPLICATION NUMBER: 60/047,617

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R APPLICATION NUMBER: 60/047,618

R FILING DATE: 1997-05-23

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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,632
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APPLICATION NUMBER: 60/040,336
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APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,581
FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
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R APPLICATION NUMBER: 60/043,669
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,312
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,313
R APPLICATION NUMBER: 60/043,672
R R PILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,415
R R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,415
R R FILING DATE: 1997-04-11 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 PLICATION NUMBER: 60/056,845 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,893 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 APPLICATION NUMBER: 60/056,880 APPLICATION NUMBER: 60/056,636 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/043,580 1997-08-22 1997-08-22 FILING DATE: 1997-08-22 1997-08-22 FILING DATE: 1997-08-22 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: FILING DATE: FILING DATE: LING DATE: LING DATE: EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER SARLIER EARLIER EARLIER EARLIER

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Sequence 72.7. Application US/09949016
; Sequence 72.7. Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VBNTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WINDER: US/09/949,016
; CURRENT PILLING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-010-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-010-03
; PRIOR SPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-010-03
; PRIOR FILING DATE: 2000-010-03
; PRIOR SPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-010-03
; PRIOR FILING DATE: 2000-010-03
; PRIOR FILING DATE: 2000-010-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-010-03
; PRIOR FILING DATE: 2000-04-04
; PRIOR FILING DATE: 2000-04-04-04
; PRIOR FILING DATE: 2000-04-04
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                                                                                                                                                                      241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLFSKEEPVNTVYS 300
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TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                            121 TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVBKBEKNVTYNWSPLGEBGNVLQI
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100.0%; Pred. No. 3.6e-166;
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Best Local Similarity 100.
Matches 328; Conservative
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ORGANISM: Human
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US-09-949-016-6907
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US-09-949-016-7327
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99.9%; Score 1695; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.5e-166;
Matches 328; Conservative 0; Mismatches 0;
                                                                                               EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-2
                                     R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/047,595

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,588

R APPLICATION NUMBER: 60/047,588

R APPLICATION NUMBER: 60/047,585

R APPLICATION NUMBER: 60/047,585
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CLASSIFICATION: 33.0

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX

TELECOMMUNICATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415-496-1200
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STATE: California
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                                                                                      Query Match
Best Local Similarity
Matches 85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                  ORGANISM: Human
US-09-949-016-7325
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US-08-348-792-8
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patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NO 7225
                                     APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 05/241,755
PRIOR APPLICATION NUMBER: 66/241,755
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLING APPLICATION NUMBER: 66/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOCTHARB: FaetSEQ for Windows Version 4.0
LENGTH: 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GFHHILKWENGSLPSNTSN-----DRFSFIVKNLSLLIKAAQQQDSGLYCLEV-TSISGK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 -FWPFLVIIVILSALFLGTLACFCVWRRKRKBKQSETSPKEFLTIYEDVKDLKTRRNHEQ 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 SVAYVIPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTOADPY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 TITKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW----SPLGEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNVLQIFQIPEDQEL----TYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 VLAMFFLLVLILSSVFLFRLF-----KRRQDAASKK---TIYTYI--MASRNTQPA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ILLILLKVYQGKGCQGSADHVVSISGV-----PLQLQPNSIQTKVDSIAWKKLLPSQN 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ILLLCLQTW---PEAAGKDSEIFTVNGILGESVTFPVNIQE---PRQVKIIAW----TSKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.4%; Score 227; DB 4; Length 365
23.6%; Pred. No. 1e-14;
ive 65; Mismatches 142; Indels
6907, Application US/09949016
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Best Local Similarity 23.6
Matches 85; Conservative
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US-09-949-016-7325
                            Patent No. 68123.
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59 SVAYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08348792
Patent No. 5576423
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL AVERSA, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Ge Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURPACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                             68;
        Length 391;
13.4%; Score 227; DB 4; Length 39 ilarity 23.6%; Pred. No. 1.1e-14; Conservative 65; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
DATHORNIN: S30
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901 California Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Gaps

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71 YLE-----NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 119
                                                                                                                                                                                                                                                                   81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
                                                                                                                                                                                                                                                                                                                                                     139 OSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 190
                                                                                                                                                                                                                                                                                                                                                                               120 VLNKTQENGTCTLILGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 SVFLFRLFKRR-----QDAASKKTIYTYIMASR-----NTQPAE---SRIYDEILQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 YTCTAQNPVSNNSDSISARQLCADIAMGFRTH------HTGLLSVLAMFFLLVLILS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 IGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 70
                                                                                                                                                                                    33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
                                                                                                                                          78;
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APPLICANT: Aversa, Gregorio

APPLICANT: Chang, Chia-Chun J.

APPLICANT: Cocks, Benjamin G.

APPLICANT: de Vries, Jan E.

TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL

TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES

NUMBER OF SQUENCES: 12

CORRESPONDENCE ANDRESS:
                                                                                              11.4%; Score 194; DB 2; Length 307; 23.8%; Pred. No. 1.9e-11; Live 54; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-JUN-1995
APPLICATION UNBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
FELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/199,955 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 SKVLPSKEEPVN--TVYSEV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
               linear
amino acid
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US-08-462-738-8
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                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                              120 VLNKTQENGTCTLILGCTVEKGD-HVAYSWSERAGTHPLNPANSSHLLSLTLGPQHADNI 178
                                                                                                                                                                                                                                                                                                                                                                                                                               81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
                                                                                                                                                                                                                                                                                                                    139 OSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 190
                                                                                                                                                                                                                                                                                                                                                                                                       191 YTCTAQNPVSNNSDSISARQLCADIAMGFRTH------HTGLLSVLAMFFLLVLILS 241
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                                                                                                                                                                                11 LGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPFRYLGDRYKF 70
                                                                                                                                                 33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN 80
                                                                                                         Gaps
                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Aversa, Gregorio
APPLICANT: Canay, Cria-chun J.

APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.

TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES

TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
                                                               Length 307;
                                                                                                         112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
                                                               11.4%; Score 194; DB 1;
23.8%; Pred. No. 1.9e-11;
iive 54; Mismatches 112
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CLASSIPICATION DATA:
APPLICATION NUMBER: 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GB
TELECPHONE: 415-852-9196
TELEPHONE: 415-852-9196
TELEFRAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 8:
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ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 SKVLPSKEEPVN--TVYSEV 302
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Patent No. 5977303
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                                                                               Best Local Similarity 23.8%
Matches 76; Conservative
    MOLECULE TYPE: protein
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STATE: California
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           ; MOLECULE 13
US-08-348-792-8
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REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
RAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,0
                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                        81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
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                                                                                                                                                                                                                                                  33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN 80
                                                                                                                                                                                                                                                                           11 LGSKVLLPLTYERINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSBAGPPRYLGDRYKF 70
                                                                                                                                                                                                                 Gaps
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                 78;
                                                                                                                                                                        11.4%; Score 194; DB 3; Length 307;
23.8%; Pred. No. 1.9e-11;
ive 54; Mismatches 112; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
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ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PLOPSY DISK
MEDIUM TYPE: PLOPSY MS-DOS
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901 California Avenue
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/348,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-DEC-1994
VITORNEY/AGENT INFORMATION:
NAME: Ching FALL:
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Patent No. 6399065
     TELEFAX: 415-496-1200
INFORMATION FOR SEX ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acids
                                                                                                                                                                        Query Match
Best Local Similarity 23.8<sup>1</sup>
Matches 76; Conservative
                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: California
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US-08-880-875-8
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81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
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                                                                                                                                                                               11 LGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 70
                                                                                                                        33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
                                                             78; Gaps
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Sequence 2, Application US/08348792;
Patent No. 5576423
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Govers, Benjamin G.
TITLE OF INVENTION: PURFIFED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES;
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
Length 307;
Query Match 11.4%; Score 194; DB 3; Length 30
Best Local Similarity 23.8%; Pred. No. 1.9e-11;
Matches 76; Conservative 54; Mismatches 112; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 92/08/348,792
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99 YLE-----NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 -----LRRRGKTNHYQTTVEKKSLTIYAQVQKPGPLQKKLDSFPAQDPCTTIY--VAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 LGESVTFP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
TITLE OF INVENTION: BURFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.4%; Score 194; DB 2; Length 335; 23.8%; Pred. No. 2.2e-11;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Mismatches 112;
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APPLICATION NUMBER: US 08/461,473
                                                                               DX0436GB
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APPLICATION NUMBER: US/09/199,955
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NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                  TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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STATE: California
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-462-738-2
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Sequence 2, Application US/08462738

Sequence 2, Application US/08462738

Patent No. 5977303

GENERAL INFORMATION:

APPLICANT: Chang, Chia-Chun J.

APPLICANT: Cocks, Benjamin G.

APPLICANT: Cocks, Benjamin G.

TITLE OF INVENTION: PURIFIED GENES ENCODING MANMALIAN CELL

TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES;

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%; Score 194; DB 1; Length 335; 23.8%; Pred. No. 2.2e-11; tive 54; Mismatches 112; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
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901 California Avenue
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                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEPAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
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APPLICATION NUMBER: US 0
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.4%;
Best Local Similarity 23.8%;
Matches 76; Conservative
                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                               : 335 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                            TOPOLOGY:
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81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
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APPLICANT: Young, Paul
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation
TITLE OF INVENTION: Molecule
FILE REFERENCE: PF448P1
CURRENT APPLICATION NUMBER: US/09/369,248A
CURRENT FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: 60/073,962
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
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                          PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-UNN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
TELEPHONE: 415.852-9196
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amino acid
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Best Local Similarity 23.8*
Matches 76; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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SOFTWARE: Patentin Ver. SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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ORGANISM: Homo sapiens
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US-09-369-248A-3
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GENERAL INFORMATION:
APPLICANT: Averagorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: We Vries, Jan E.
TITLE OF INVENTION: FURLFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                             Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                        11.4%; Score 194; DB 3; Length 33 23.8%; Pred. No. 2.2e-11; tive 54; Mismatches 112; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
           APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 12
CORRESPONDENCES.
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
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Patent No. 6399065
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 335 antho acids TYPE: amino acid TOPOLOGY: linear
05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 23.8
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STATE: California
COUNTRY: USA
ZIP: 94104-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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US-08-880-875-2
                                                                                                                                                                                                                                                                                                                                                                    US-09-199-955-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 YLE-----NITLGIRESRREDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 YTCTAONPVSNNSDSISARQLCADIAMGFRTH------HTGLLSVLAMFFLLVLILS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 YICTVSNPISNNSQTFSPWPGC-----RTDPSETKPWAVYAGLLGGVIMILIMVVILQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | || : | |: | : | |: || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 
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                                                                                                                                                                                                                                                                                                                                                                                                                        39 LGSKVLLPLTYERINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 98
                                                                                                                                                                                                                                                                                                                                       33 LGESVTFP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN 80
                                                                                            Query Match
11.4%; Score 194; DB 4; Length 335;
Best Local Similarity 23.8%; Pred. No. 2.2e-11;
Matches 76; Conservative 54; Mismatches 112; Indels
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZOLOP1
CURRENT APPLICATION NUMBER: US/09/227,357
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EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
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EARLIER APPLICATION NUMBER: 60/051,926
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/052,803
FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,932
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APPLICATION NUMBER: 60/051,930
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FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/051,916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 SKVLPSKEEPVN--TVYSEV 302
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US-09-369-248A-3
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60 VAYVIPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINIQADPYT 119
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (143)
OTHER INFORMATION: Xaa equals stop translation
                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
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EARLIER FILING DATE: 1997-09-12
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APPLICATION NUMBER: 60/055,948
FILING DATE: 1997-08-18
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APPLICATION NUMBER: 60/055,947
FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
                                                                                                                                                                              APPLICATION NUMBER: 60/055,953
                                                                                                                               APPLICATION NUMBER: 60/055,949
                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/055,950
                        APPLICATION NUMBER: 60/055,723
                                                                                                                                                                                                                FILING DATE: 1997-08-18
1997-08-18
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ORGANISM: Homo sapiens
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Matches 44; Conserv
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NAME/KEY: SITE
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LOCATION: (138
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Search completed: February 4, 2005, 12:17:03 Job time : 39.0095 secs

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February 4, 2005, 12:15:12; Search time 108.42 Seconds (without alignments) 988.338 Million cell updates/sec
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1 MAQHHLWILLLCLQTWPEAA.......KASTQDSKPPGTSSYEIVIX 329
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SUMMARIES

Sequence 30, Appl Sequence 483, App Sequence 483, App Sequence 483, App Sequence 8 Sequence 4 Description US-10-104-943-4 US-10-446-523-30 US-09-809-391-483 US-09-882-171-483 US-10-164-861-483 US-10-1471-49-8 US-10-10-860-836B-11 US-10-10-943-7 US-10-328-538-2 US-10-328-538-2 US-10-328-538-2 US-10-328-538-2 US-10-328-538-2 US-10-338-538-2 US-10-338-538-2 US-10-338-538-2 US-10-338-538-2 US-10-338-538-2 * Query Match Length DB Score 1695 1695 1695 1695 382.5 382.5 374 374 373 373 Result 80.

8, Appli 11, Appl 2, Appli 2, Appli 18, Appli 76, Appl

Sequence Sequence Sequence Sequence

Sequence 1 Sequence 7 Sequence 2

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US-10-436	10-436-523-	US-10-436	US-10-436-523-	US-10-436-523-	US-10-257-174-	US-09-732	US-09-989-722-	723-	US-09-989-279-25	US-09-989-727-	989-731-25	US-09-989-732-25	9 US-09-745-605-4	9 US-09-991-073-253	9 US-09-990-442-253	9 US-09-991-163-253	9 US-09-993-604-253	9 US-09-990-456-253	-Sn	US-09-992-598-25	989-293A	US-09-989-735-25	990-444-25	991-181-	US-09-989-730-25	-980-436-	US-09-993-687-25	US-09-989-734-2	997-653-25	0 US-09-989-724-2	0 US-09-989-728-2
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370	370	370	369	367	363.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5	362.5
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ALIGNMENTS

RESULT 1 US-10-104-943-4 US-10-104-943-4 Sequence 4, Application US/10104943 Sequence 4, Application US/10104943 Sequence 4, Application US/20030092017A1 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENT	ING A NOVEL IMMUNOGLOBULIN SUPERFAMILY MEN LICE VARIANTS THEREOF 3	змве.
Query Match 99.9%; Score 1695; DB 14; Best Local Similarity 100.0%; Pred. No. 2e-144; Matches 328; Conservative 0; Mismatches 0;	5, DB 14; Length 328; . 2e-144; ches 0; Indels 0; Gaps 0;	
Qy 1 MAQHHIMILILCLQTWPEAAGKDSELFTVNGILGESVTFPVNIQEPROVKIIAMTSKTSV	NGILGESVTFPVNIQEPROVKIIAMTSKTSV 60 	
Qy 61 AYVIEGDSETAPVVIVIHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 	PNYNLVISDLRMEDAGDYKADINTQADPYTT 120 	
Qy 121 TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI 180	NVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI 180	

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LENGTH: 329
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100.0%; Pred. No. 2e-144;
iive 0; Mismatches 0;
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US-10-436-523-30
Sequence 30, Application US/10436523
; Publication No. US20030180888A1
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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US-09-809-391-483
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Sequence 483, Application US/09809391 Publication No. US20030049618A1 GENERAL INFORMATION: APPLICANT: Ruben et al.

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241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 329;
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.9%; Score 1695; DB 10;
100.0%; Pred. No. 2.1e-144;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (329)
OTHER INFORMATION: Xaa equals stop translation
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FILE REPERENCE: P2002P2
CURRENT APPLICATION 186 Human Secreted prote:
FILE REPERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-00-08
PRIOR FILING DATE: 1998-00-07
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR APPLICATION NUMBER: 60/040,163
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
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Matches 328; Conservative
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                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
LOCATION: (329)
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R APPLICATION NUMBER: 60/043,672 R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/043,315 R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/048,974 R FILING DATE: 1997-06-06 R APPLICATION NUMBER: 60/047,596
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,596
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,612
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,632
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R PILING DATE: 1997-05-30
R PILING DATE: 1997-04-11
R PILING DATE: 1997-04-11
R PILING DATE: 1997-04-11 REFLICATION NUMBER: 60/043,314

R APPLICATION NUMBER: 60/043,314

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,569

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R APPLICATION NUMBER: 60/043,311 R FILING DATE: 1997-04-11
R PAPLICATION NUMBER: 60/043,674
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,669
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,312
R FILING DATE: 1997-04-11 R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,617
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R FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,502 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,583 APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,500 APPLICATION NUMBER: 60/040,163 FILING DATE: 1997-03-07 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-03-07 PRIOR
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/057,761 R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,880
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/047,595
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,599
FILING DATE: 1997-05-23 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,589
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 APPLICATION WUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 APPLICATION NUMBER: 60/047,588 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,585 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-08-22 APPLICATION UNDBER: 60/056,636 ELING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,893
FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22
APPLICATION UNDBER: 60/056,872
APLING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,882 ILING DATE: 1997-08-22 PPLICATION NUMBER: 60/056,877 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 1997-05-23 FILING DATE: PRIOR

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                                                                                                                                                                                                                                                                                                Length 329;
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APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
APPLICANT: TANG, Y. TOM, DUGGAN, Brendan M.;
APPLICANT: TRAN, UYEN K.; BAUGHN, Mariah R.;
APPLICANT: HONCHELL, Cynthia D.; BURFORD, Neil;
APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
APPLICANT: MASON, Patricia M.
TITLE OF INTENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-0925 USN
                                                                                                                                                                                                                                                                                                   99.9%; Score 1695; DB 15;
100.0%; Pred. No. 2.1e-144;
tive 0; Mismatches 0;
                                                                                                                                                                NAME/KEY: SITE
LOCATION: (329)
COTHER INFORMATION: Xaa equals stop translation
US-10-164-861-483
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CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: US/10/471,449

CURRENT FILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-03-12

PRIOR PLING DATE: 2001-03-12

PRIOR PLING DATE: 2001-03-12

PRIOR PLING DATE: 2001-08-31

PRIOR PLING DATE: 2001-08-31

PRIOR PLING DATE: 2001-08-31

PRIOR PLING DATE: 2001-09-21

PRIOR PLING DATE: 2001-09-21

PRIOR PLING DATE: 2001-09-21

PRIOR PLING DATE: 2001-10-26

PRIOR PRIOR DATE: 2001-10-26

PRIOR PRIOR PRIOR NUMBER: US 60/343,880

PRIOR PRING DATE: 2001-11-02

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PRED PROGRAM
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                  PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 328; Conservative
NUMBER OF SEQ ID NOS: 757
                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                  SOFTWARE: Pat
SEQ ID NO 483
LENGTH: 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.9%; Score 1695; DB 10; Best Local Similarity 100.0%; Pred. No. 2.1e-144; Matches 328; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence (483, Application US/10164861
Publication No. US20030225248A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-03-06
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             PRIOR APPLICATION NUMBER: 60/043,670
PRIOR FILING DATE: 1997-04-11
PRIOR PELING DATE: 1997-04-11
PRIOR PELING DATE: 1997-04-22
PRIOR FILING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,816
PRIOR PELING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,816
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
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PRIOR PELING DATE: 1997-06-05
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-05
PRIOR PELING DATE: 1997-08-05
PRIOR PELING DATE: 1997-08-05
PRIOR PELING DATE: 1997-08-05
FILING DATE: 1997-05-23
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US-09-660-836B-11

US-09-660-836B-11

Sequence 11, Application US/09860836B

Publication No. US20030054002A1

GENERAL INFORMATION:
APPLICANT: WAKELAND, WARD

APPLICANT: WANDELLANTON: AMY

APPLICANT: WANDELLOANTON USEL, LANDENCE,
TITLE OF INVENTION: IN IMMUNE TOLERANCE

TITLE OF INVENTION: IN IMMUNE TOLERANCE

CURRENT PELLOCATION UNMBER: US/09/860,836B

CURRENT FILING DATE: 2002-08-13

FRIOR APPLICATION NUMBER: 60/204,963

PRIOR PELLOATION NUMBER: 60/204,963

NUMBER OF SEQ ID NOS: 37

SOFTWARE PATENTING DATE: 2000-09-21

NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                          FARPKEN-----VTIMVKSYLGRLDITKWSYSLCISNLTLNDAGSYKAQINQRNFEVTTE 143
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                                                                                                                                                                                                                       3 OHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTS-KTSVA
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22.6%; Score 382.5; DB 10; Length 610;
Best Local Similarity 33.9%; Pred. No. 1.5e-25;
Matches 101; Conservative 60; Mismatches 100; Indels 37;
                                                                                                                                        DB 15; Length 551;
                                                                                                                                      Query Match 22.6%; Score 382.5; DB 15; Length Best Local Similarity 33.9%; Pred. No. 1.3e-25; Matches 101; Conservative 60; Mismatches 100; Indels
                                                       NAME/KEY: misc feature
CTHER INFORMATION: Incyte ID No: 7500099CD1
US-10-471-449-8
                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapien
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LENGTH: 610
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Sequence 7, Application US/10104943

Publication NO. US20030092017A1

GENERAL INFORMATION:

TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF

TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF

TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF

FILE REFERENCE: D0135 NP

CURRENT APPLICATION NUMBER: US/10/104,943

CURRENT APPLICATION NUMBER: US 60/278,037

PRIOR APPLICATION NUMBER: US 60/278,037

PRIOR PLING DATE: 2001-03-22

PRIOR PLING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 129

SOFTWARE: Patentin version 3.0

SEQ ID NO 7.
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US-10-510-612-2

US-10-310-612-2

y publication No. US20040109862A1

GENERAL INFORMATION:

APPLICANT: Entage, Peter

TITLE OF INVENTION: that express Ly-9

TITLE OF INVENTION that express Ly-9

TITLE OF INVENTION NUMBER: US/10/310,612

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.1

SEQ ID NO 2.
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                                                           232 MFFLLVLILSS------VFLFR---LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
                                                                                          | | | : | : | : | : | : | : | 3.2 EPUTLPLALPACRDTEKVVWLFNTSIISKERBEAATADPLI-----KSRDFYKNRVW 283
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22.1%; Score 374; DB 14; Length 65:
Best Local Similarity 33.0%; Pred. No. 9.9e-25;
Matches 98; Conservative 59; Mismatches 104; Indels
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US-10-310-612-2
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ORGANISM: Homo sapiens
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US-10-436-523-76
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TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of cells
TITLE OF INVENTION: that express Ly-9
FILE REPERBNCE: HYS-68CP
CURRENT APPLICATION NUMBER: US/10/328,538
CURRENT FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
                                                                                                                                                                           89 FARPKEN-----VTIMVKSYLGRLDITKWSYSLCISNLTLNDAGSYKAQINQRNFEVTTE 143
                                                                                                                                                                                                                              KRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEEG 175
                                                                                                                                                                                                                                                  NVLQIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLAM 232
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                                                                            3 QHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA 61
                                                                                                           33 OTSLLFLLMGLR----ASGKDSAPTVVSGILGGSVTLPLNISVDTEIENVIWIGPKNALA 88
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22.1%; Score 374; DB 16; Length 654; ilarity 33.0%; Pred. No. 9.9e-25; Conservative 59; Mismatches 104; Indels 30
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US-10-328-538-2
'Sequence 2, Application US/10328538
'Publication No. US20040109863A1
'GENERAL INFORMATION:
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Best Local Similarity 33.0
Matches 98; Conservative
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ORGANISM: Homo sapiens
Query Match
Best Local Similarity
Matches 98; Conserv?
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US-10-328-538-2
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RESULT 11

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APPLICANT: No. US20030124575Alartis AG
APPLICANT: No. US20030124575Alartis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: Phares, William
APPLICANT: Werner, Gudrun
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Publication No. US20030180888A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fraser
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
FILE REFRENCE: 7633-244-999
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: US/10/007,303
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 100
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                                                                                                           APPLICANT: NO. US20030124575Alartis As APPLICANT: NO. US20030124575Alartis Erfindungen Verwaltung APPLICANT: Phares, William APPLICANT: Wenner, Gudrun APPLICANT: Wenner, Gudrun APPLICANT: Jartz, Markus APPLICANT: Lapp, Hilmar APPLICANT: Lapp, Hilmar TITLE OF INVENTION: Organic Compounds FILE REFERENCE: 4.31347 PCT CURRENT APPLICATION NUMBER: US/10/220,946 CURRENT FILING DATE: 2002-99-06.

PRIOR PPLICATION NUMBER: US 60/192,934 PRIOR FILING DATE: 2000-05-18 PRIOR PLICATION NUMBER: US 60/205,026 (US 60/279,243) PRIOR FILING DATE: 2000-05-18 PRIOR APPLICATION NUMBER: US 60/205,769 PRIOR FILING DATE: 2000-05-19 PRIOR PILING DATE: 2000-05-19 NUMBER OF SEQ IO NOS: 22 SOFTWARE: PRESEQ For Windows Version 4.0
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Sequence 18, Application US/10220946 Publication No. US20030124575A1 GENERAL INFORMATION:
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60 VAYVIPGDSETAPVVIVIHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINIQADPYT 119
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                                                              EGNVLQIFQTPEDQELTYTCTAQNPVSN-NSDSISARQLCADIAMGFRTHHTG---LLSV 229
                                                                                                                                           7 WILLLCL-----QTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTS
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                                       TTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGE----
                                                                                                                                                                                                                                                                                                                                   ; Sequence 88, Application US/10436523; publication No. US20030180888A1; publication No. US2003018088BA1; publication No. US2003018088BA1; publication No. US200301808BA1; publication No. US200301808BA1; papelICANT: Fraser, Christopher C.; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF; TILE REFERENCE: 7853-244-999; CURRENT APPLICATION NUMBER: US/10/436,523; CURRENT FILING DATE: 2003-05-12; PRIOR APPLICATION NUMBER: US/10/007,303; PRIOR PILING DATE: 2000-11-03; NUMBER OF SEQ ID NOS: 100; NUMBER OF SEQ ID NOS: 100; SOFTWARE: Patentin version 3.1
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; Publication No. US20030180888A1
; GENERAL INFORMATION:
   APPLICANT: Fraser, Christopher C,
   TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
   FILE REFERENCE: 7853-244-999
; CURRENT APPLICANT ON UMBER: 2003-05-12
; FILE REPERENT FILING DATE: 2003-05-12
; FRIOR APPLICATION NUMBER: US/10/007,303
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Best Local Similarity 31.7%; Pred. No. 7.2e-25;
Matches 91; Conservative 55; Mismatches 119;
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US-10-436-523-88
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US-10-436-523-89
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US-10-436-523-88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 LLIFILLVILAMGLWVIRVQKRHKMPRMKKLMRNRMKLRKEAKPGSS 287
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                                                                                                                                                                                       54; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kingsman, Susan Mary
APPLICANT: Kinge, David
TITLE OF INVENTION: ANALYSIS METHOD
TITLE OF INVENTION: ANALYSIS METHOD
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR PILING DATE: 2001-04-08
PRIOR PLILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christopher Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 131, Application US/10170385 Publication No. US20030203372A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White, Jonathan
Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mundy, Christopher R
Kan, On
Harris, Robert Alan
        SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ward, Neil Raymond
                                                                                                                                                  Query Match
Best Local Similarity 32.1%
Matches 92; Conservative
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                                                                                     ORGANISM: Homo sapiens
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SEQ ID NO 131
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                             SEQ ID NO 76
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 EGNVIQIFQTPEDQELTYTCTAQNPVSN-NSDSISARQLCADIAMGFRTHHTG---LLSV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 EGPVLSTSWRPGDSALSYTCRANNPISNVSSCPIPDGPFYADPNYASEKPSTAFCLLAKG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.8%; Score 370; DB 14; Length 289; Best Local Similarity 31.7%; Pred. No. 7.2e-25; Matches 91; Conservative 55; Mismatches 119; Indels 22;
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; PRIOR FILING DATE: 2001-11-20; PRIOR APPLICATION NUMBER: 09/706,167; PRIOR FILING DATE: 2000-11-03; NUMBER OF SEQ ID NOS: 100; SOFTWARE: Patentin version 3.1; SEQ ID NO 89; LENGTH: 289; TYPE: PRT (CREATER PATE) (CREATER PATE) (CREATER PATE) (CREATER PRT) (CREATER PATE) (CREATE) (CREATER PATE) (CREATE) (CREATER PATE) (CREATER PATE) (CREATER PATE) (CREATER PATE) (
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Search completed: February 4, 2005, 12:32:17 Job time : 110.42 secs

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GenCore version 5.1.6
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2005, 12:03:57 ; Search time 31.7784 Seconds	(without alignments)	996.126 Million cell updates/sec
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US-09-882-171-483 1696 1 MAQHHLWILLLCLQTWPEAA.........KASTQDSKPPGTSSYEIVIX 329 Title: Perfect score: Sequence:

BLÓSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dю				
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
-	336	19.8	629	2	A46500	Ly-9.2 antigen - m
8	194	11.4	335	~	S58892	signaling lymphocy
m	180	10.6	240	~	801299	OX-45 membrane gly
4	179.5	10.6	240	~	JL0143	BCM1 p
S	164	9.7	398	~	I49443	gene 2B4 protein -
9	143.5	8.5	521	~	S34338	
7	142.5	8.4	458	-	WMMSR1	
80	142.5	8.4		7	JC1508	➣
6	141.5	8.3	347	~	S41638	
10	139.5	8.2	458	7	JC1509	biliary glycoprote
11		8.1	518	7	JC4024	poliovirus recepto
12	137	8.1	351	Н	RWHUC2	T-cell surface gly
13	135.5	8.0	702	~	A36319	carcinoembryonic a
14	134.5	7.9	417	Н	RWHUPA	poliovirus recepto
15	131.5	7.8	344	~	A27681	nonspecific cross-
16	127.5	7.5	344	~	B28967	T-cell surface gly
17	127.5	7.5	392	٦	RWHUPD	poliovirus recepto
18	125	7.4	338	~	JC4776	limbic-system-asso
19	124.5	7.3	519	~	A44783	ecto-ATPase precur
20		7.3	417	~	A44194	poliovirus recepto
21		7.2	321	~	JH0395	biliary glycoprote
22	122.5	7.2	351	7	JH0396	biliary glycoprote
23		7.2	417		JH0394	biliary glycoprote
24	122.5	7.2	464	7	C30127	transmembrane carc
25	122.5	7.2	526	н	A32164	biliary glycoprote
56	121.5	7.2	338	7	JC1238	oid-bindi
27	121.5	7.2	344	7	I49585	CD2 antigen protei
28	121.5	7.2	345	~	803199	opioid-binding pro
29	121.5	7.2	345	~	JC1239	opioid-binding pro

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carcinoembryonic a opioid-binding cel	SOK GIYCOPIOUEIN P neurotrimin - rat pregnancy-specific preenancy-specific	pregnancy-specific biliary glycoprote pregnancy-specific	pregnancy-specific pregnancy-specific pregnancy-specific	pregnancy-specific pregnancy-specific pregnancy-specific pregnancy-specific
A55811 JC4025	JC5519 156551 A28277 A33258	B33258 JC1511 JC4123	D43354 C43354 E43354	A31135 A35964 A35341 A27658
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ALIGNMENTS

RESULT 1 A46500

Ly-9.2 antige C,Species: Mu C,Date: 18-Ju	Ly-9.2 antigen - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C, Accession: A46500 R; Sandrin, M.S.; Gun	A46500 S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.
A;Title: Isol	 Immunol. 149, 1636-1641, 1594 AjTitle: Isolation and characterization of cDNA clones for mouse Ly-9. Defendence number. 146500. MITD:92171005; PMID:1506686
A; Accession: A46500	A46500
A; Molecule type: mRNA;	A; Occours: First minA; protein A; Molecule type: minA; protein A; Designer: 1-679 . Can.
A; Cross-refer	A; Cross-references: GB: M84412; NID: g198931; PIDN: AAA39468.1; PID: g198932
A; Experimenta A; Note: seque C; Keywords: t	A,Experimental source: C57BL/6 A,Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654) C,Keywords: transmembrane protein
Query Match	19.8%; Score 336; DB 2; Length 629;
Best Local Matches 10	Best Local Similarity 24.7%; Pred. No. 3.4e-19; Matches 100; Conservative 55; Mismatches 136; Indels 114; Gaps 7;
Qy 19	19 AAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTH 78
Db 230	
Qy 79	79 RNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKIT 138
Db 285	GSEERRVRTSDQDQSLKISQLKMEDAGPYHAYVCSEASRDPSVRHFTLLVYKRLEKPSVT 344
0y 139	139 QSLMASVNSTCNVTLTCSVEKEEKAVTYNWSPLGEEGNVLQIFQTPEDQELTYT 192
Db 345	S KSPVHMMIGICEVVLTCSVDGGGNNVTYTMMPLQNKAVMSQGKSHLNVSWESGEHLPNFT 404
Qy 193	CTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLILSSVFLFRLFKR- 251
Db 405	CTAHNPVSNSSQFSSGTICSGPERNKRFWLLLLLVLLLLMLIGGYFILRKKKQC 459
Qy 255	252 RODAASKKIIYTYIMAS 268
Db 46() SSLATRYRQAEVPAEIPEPPTGHGQFSVLSQRYEKLDMSAKTTRHQPTPTSDTSSESSAT 519
Qy 269)RNTQPAESRIYDEILQSKV 287
Dp 25(: ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::

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A, Residues: 1-240 < WON>
A, Cross-references: UNIPROT: P18181; EMBL: X17501; NID: 950134; PIDN: CAA35542.1; PID: 950135. R; Wong, Y. W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
submitted to the EMBL Data Library, June 1990
A, Description: Structure, expression and genetic linkage of the mouse BCMI (OX45 or Blass) a region on mouse chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sgp-60 as the m
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A.Note: sequence extracted from NCBI backbone (NCBIP:129660)
C.Comment: This antigen is widely expressed on leukocytes and is likely to be anchored to C.Comment: This antigen is widely expressed on leukocytes and is likely to be anchored to C.Superfamily: B-cell surface glycoprotein blast-1
C.Superfamily: B-cell surface glycoprotein; lipoprotein; phosphatidylinositol linkac, F:1-22/Domain: signal sequence #status predicted <ANTO-F:1-21/Product: antigen BCMI #status predicted <ANTO-F:210-210/Product: antigen BCMI #status predicted <ANTO-F:210-240/Domain: carboxyl-terminal propeptide #status predicted <CPTO-F:32.38.70,136.186.203/Binding site: carbohydrate (Asn) (covalent) #status predicted F:217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen BCM1 precursor - mouse

N;Alternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0043; S21319; Ā47469; B47469
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
A;Exp. Med. 171, 2115-2130, 1990
A;Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1) region on mouse chromosome 3.
A;Reference number: JL0143; MUID:90278362; PMID:1693656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                      179 QIFQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVL 238
GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGD-YKADINTQADPYTTTKRY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 WILLLCLQTWPEAAG-KDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTSVAYVTP 65
                                                                                                                                                                                                                                                                                                                                                                                                                           :| || :: || || || || || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || 
                                                                                       71 GKK----TVFESVFKDRVDLDKTNGALRIYNVSKEDRGDYYMRMLHETEDQWKIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A; Residues: 1-240 < WOND.

A; Residues: 1-240 < WOND.

A; Cross-references: ENGL: X53526; NID: 950138; PIDN: CAA37604.1; PID: 950139

R; Cabrero, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.

R; Cabrero, J.G.; Freeman, G.J.; Jane, W.S.; Reiser, H.

A; Cabrero, J.G.; Protein sequencing and gene transfection, of

A; Reference number: A47469; MUID: 93234508; PMID: 8475091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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A;Note: sequence extracted from NCBI backbone (NCBIP:129658)
A;Accession: B47469
                                                                                                                                                                                       125 NLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.6%; Score 179.5; DB 2; 23.6%; Pred. No. 4.3e-07; ative 47; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 ILSSVFL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: |: |
IIPSILL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 84-98 < CA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JL0143
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OX-45 membrane glycoprotein precursor - rat

NyAlternate names: MRC OX-45 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01299
R;Killeen, N.; Mossaner, R.; Arvieux, J.; Willis, A.; Williams, A.F.
EMBO J. 7, 3087-3091, 1988
A;Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the i
A;Reference number: S01299; MUD:89030603; PMID:3181129
A;Accession: S01299
A;Molecule type: mRNA
A;Residues: 1-240 < KIL>
A;Cross-references: UNIPROT:P10252; EMBL:X13016; NID:956804; PIDN:CAA31438.1; PID:956805
C;Superfamily: B-cell surface glycoprotein blast-1
C;Keywords: glycoprotein; membrane protein; surface antigen
F;1-22-CDomain: signal sequence #status predicted < ASIG>
F;33-240/Product: OX-45 membrane glycoprotein #status predicted <ASIG>
F;38,97,140,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary; nucleic acid sequence not shown
A, Molecule type: mRNA
A, Residues: 1-315 - CCC>
A, Cross-references: UNIPROT: Q13291; EMBL: U33017; NID: 9984968; PIDN: AAA75380.1; PID: 99849
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                                                                                                                                                                                                                                        J.M.; Yssel, H.; de Vries, J.E.; Aversa,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 YLE-----NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 VLNKTQENGTCTLILGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 YTCTAONPVSNNSDSISARQLCADIAMGFRTH------HTGLLSVLAMFFLLVLILS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 YICTVSNPISNNSQTFSPWPGC-----RTDPSETKPWAVYAGLLGGVIMILIMVVILQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 SVFLFRLFKRR-----QDAASKKTIYTYIMASR-----NTQPAE---SRIYDEILQ 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
                                           gnaling lymphocytic activation molecule - human
Species: Homo sapiens (man)
Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 LGESVTFP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGSKVLLPLTYERINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF
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                                                                                                                                                                                       C;Accession: S58892
R;Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Yssel, H.;
Nature 376, 260-263, 1995
A;Title: A novel receptor involved in T-cell activation.
A;Reference number: S58892; MUID:95342241; PMID:7617038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.4%; Score 194; DB 2; Le Best Local Similarity 23.8%; Pred. No. 4.5e-08; Matches 76; Conservative 54; Mismatches 112;
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Matches 62; Conserv
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N;Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C;Species: Wus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 534338, JC1510; A41093
R;Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
submitted to the EMBL Data Library, July 1992
A;Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A;Reference number: 334338
A;Reterior: S34338
A;Retus: preliminary
A;Retus: preliminary
A;Residues: 1-521 * cHUA-A
A;Cross-references: UNIPROT: Q61352; EMBL: X67281; NID: 9312585; PIDN: CAA47698.1; PID: 9312
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprimitation: JC1510.
A;Accession: JC1510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AjGene: BgpF
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;354-303/Domain: immunoglobulin homology <IMM3>
F;351-396/Domain: immunoglobulin homology <IMM3>
F;31-104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the carcinoembryonic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biliary glycoprotein A precursor - mouse
NyAlternate names: carcinoembryonic antigen mmCGMla; murine hepatitis virus receptor C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-mar-1993 #text_change 09-Jul-2004
C;Date: 31-mar-1993 #sequence revision 31-mar-1993 #text_change 09-Jul-2004
C;Accession: JCL505; A49006; A4153; S11626; S11625
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Status: preliminary
A, Molecule type: protein
A, Residues: 35-59 <WIL>
C, Comment: This protein is expressed at the cell surface and plays a determinant
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 NLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 VTFPVNIQEPRQVKIJAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHA----LGPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLLIQRVIVKDTGVYTIEM-TDENFRRTEATVQFHVHQLLLKPNITSNNSNPVEGDDSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LICDSYTDPDNITYLWSRNGESLSEGDRLKLSEGNRTLTLLNVTRNDTGPYVCETRNPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAQHHL-----WILLL----CLQTW-------PEAAGKDSEIFTVNGILGES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Modecule type: mRNA
A; Residues: 1-81, '0', 83-141,'P', 143-521 <MCC>
A; Residues: 1-81, '0', 83-141,'P', 143-521 <MCC>
A; Crose references: Gs. 83-141, 'P', 143-521 <MCC
R; Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A; Title: Receptor for mouse hepatitis virus is a member (A; Reference number: A41093; MUID:91288498; PMID:1648219
A; Accession: A41093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

8.5%; Score 143.5; DB 2.
Best Local Similarity 23.8%; Pred. No. 0.00099;
Matches 59; Conservative 36; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232
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Cipture: 02-011-1996 #Requence_revision 02-011-1996 #text_change 09-011-2004
Cipture: 02-011-1996 #Requence_revision 02-011-1996 #text_change 09-011-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEL----TYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
                                                                                                                                                                                                                                                                      | ::: : | | | : : : : : : : : : : : | | LEVFDPVPKPSIEINKTEASTDSCHLRLSCEV--KDQHVDYTWYESSGPPFKKSPGYVLD 179
                                                                                                                                                                                                                                                                                                                                                                                                 QIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPED 186
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                                                                                              GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTOADPYTTTKRYN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVGVSGKPVQLRPSNIQ-----TKDVSVQW------KKTEQGSHRKIEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene 2B4 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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                                                                                                                                 126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SPLGEEGNVLQ
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                        WCLVLELLLLPLGTGFQGHSIPDINATTGSNVTLKIHKDPLGPYKRITWLHTKNQKILEY
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IHRILL 239
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Best Local S
Matches 83
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A; Molecule type: mRNA
A; Residues: 1-521 cMCC>
A; Cross-references: UNIPROT: P31809; EMBL:X67279; NID:g50170; PIDN:CAA47696.1; PID:g50171
A; Experimental source: strain CD1; tissue colon
R; Nedellec, P; Turbide, C.; Beauchemin, N.
Bur. J: Biochem. 231, 104-114, 1995
A; Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
A; Reference number: 865939; MUID:95354678; PMID:7628460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X84054; NID:g1039337
A;Experimental source: strain BALB/c
A;Experimental source: strain BALB/c
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A;Note: only a part of the coding sequence its given
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-termin C;Keywords: glycoprotein; receptor; transmembrane protein F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology «CEAN» F;160-219/Domain: immunoglobulin homology «IMM1» F;254-303/Domain: immunoglobulin homology «IMM2» F;339-336/Domain: immunoglobulin homology «IMM2» F;319-336/Domain: immunoglobulin homology «IMM3» F;11,89;104,148,199,206,210,226,258,290,294,304,317,333,375/Binding site: carbohydrate (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of mouse colon biliary glycoprc
           : |: | | | | | | | | | | BSYTDPDNINYLWSRNGESISEGDRLKLSEGNRTLTLLNVTRNDTGPYVCETRNPVSVNR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 LLVHNLPLALGAFAWYKGNTTAI----DKEIARFVPNSNMNFTGQAYSGREIIYSNGSLL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 FQMITMKDMGVYTLDM-TDENYRRTQATVRFHVHPILLKPNITSNNSNPVEGDDSVSLTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSYIDPDNINYLWSRNGESLSEGDRIKLSEGNRTLTLLLNVTRNDTGPYVCETRNPVSVNR 227
                                                                                                                                                                                                                                                                                                                                                                                                                     NiAlternate names: biliary glycoprotein 1
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence amouse)
C;Accession: JC1508; S65940; S38652
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon bilials A;Reference number: JC1505; MUID:93273228; PMID:8500759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVEKEEKNVTYNWSPLGE-----EGN-VLQIFQTPEDQELTYTCTAQNPVS-NN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 II------AWTSKTSVAYVTPGDSETAPVVTVTHRNY----YERIHALGPNYNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 ISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-21 <NED>
                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein D - mouse
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Matches 62; Conserv
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                                                                                                                                                                                                   SDPFS 232
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                                                  168
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C; Genetics:
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A; A; Recested number: A49006; MUID:92338036; PMID:1633107
A; Recested number: A49006; MUID:92338036; PMID:A433409.1; PID:953021
A; Residues: 1.458 a.MC2>
A; Cross-references extracted from NCBI backbone (NCBIN:109445; NCBIP:109446)
B; Drekeler. G. S.; Penaletro, M. N.; Cardellichio, C. B.; Williams, R. K.; Jiang, G. S.; Holme
A; Titls: Cloning of the mouse hepatitis virus (MHV) receptor: expression in human and ha
A; Reference number: A41563; MUID:92046352; PMID:1719235
A; Accession: A41563; MUID:92046352; PMID:1719235
A; Residues: 1.458 a.DVBA
A; Residues: A258 a.DVBA
A; Residues: C. Afax, D.; Afax, D.; Bell, J.; Raymond, M.; Stanners, C. P.; Fuks, A.
A; Residues: P(Y, 22-48 a.BBA
A; Rocession: S11626
A; Molecule type: mRNA
A; Residues: P(Y, 22-48 a.BBA
A; Cross-references: EMBL:X15351
B; Beauchemin, N.; Turbide, C.; Afax, D.; Bell, J.; Raymond, M.; Stanners, C. P.; Fuks, A.
A; Residues: P(Y, 22-48 a.BBA
A; Rocession: S11626
A; Molecule type: mRNA
A; Residues: S11626
A; Molecule type: MUID:9915121; PMID:2702644
A; Residues: Po; A2-214
A; Residues: S11625; MUID:9915121; PMID:2702644
A; Residues: Po; A2-31
A; Residues: Po; A2-31
A; Residues: Po; A2-31
A; Residues: Po; A2-31
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A; Residues: Po; A2-31
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A; Residues: Po; A2-31
A; Residues: Po; A2-31
A; Residues: Po; A2-31
A; Residues: Po; A2-31
A; Residues: 
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A;Reference number: UC1505; MUID:93273228; PMID:8500759
A;Accession: UC1505
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Residues: 1-458 eACC>
A;Cross-references: UNIPROT:P31809
A;Cross-references: UNIPROT:P31809
A;Cross-references: UNIPROT:P31809
A;Cross-references: UNIPROT:P31809
A;Title: mmCGM1a: a mouse carcinoembryonic antigen gene family member, generated by alter A;Reference number: A49006; MUID:92338096; PMID:1633107
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7449-485/Domain: intracellular #status predicted <CYTA.
F;71.89;104,148.152,199,206,210,226,258,290,294,304,317,333,375/Binding site: carbohydra
F;167-217,261-301,346-394/Disulfide bonds: #status predicted
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8.4%; Score 142.5; DB 1;
Best Local Similarity 25.3%; Pred. No. 0.001;
Matches 62; Conservative 27; Mismatches 103;
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poliovirus receptor-related protein precursor - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C; Accession: JC4024
R; Lopez, M; Eberle, F; Mattei, M.G; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dub Gene 155, 261-265, 1995
A; Title: Complementary DNA characterization and chromosomal localization of a human gen A; Reference number: JC4024; MUID:95237621; PMID:7721102
A, Accession: JC4024.
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F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;35-379/Domain: transmembrane #status predicted <TVM>
F;35-379/Domain: transmembrane #status predicted <TVM>
F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 YTCTAQNPVSNNSDSISARQLCADIAMGFRTH-----HTGLLSVLAMFFLVLILSSV 243
                                                                                                                                                                                                                                                                  93 NLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVT 152
                                                                                                                                                                                                                                                                                                                   LICSVEKEEKNVTYNWSPLGE-----EGN-VLQIFQTPEDQELTYTCTAQNPVS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 LTCDSYTDPDNITYLWSRNGESLSEGDRLKLSEGNRTLTLLNVTRNDTGPYVCETRNPVS 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKDSEIFTVN----SILGESVTFPVNIQEP-RQVKI--IAWT----SKTSVAYVTP--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----STCNVTLTCSVEKEEKAVTYNWSPLG-----EEGNVLQIFQTPEDQEL--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
                                                                                                                               37 VTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYYBRIHA----LGPNY
                                                        3 LASAHLHKGQVPWVGLLLTASLLASWSPPTTAEVTIEAVPPQVAEDNNVLLLVHNL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: _
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A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 INTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 -NNSDSIS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                            153
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                                                                                                     Cispecies: Equus caballus (domestic horse)
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Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q61351; GB:X67280
C;Comment: This protein is expressed at the cell surface and plays a determinant role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Asn)
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F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IMM1>
F;280-219/Domain: immunoglobulin homology <IMM2>
F;380-336/Domain: immunoglobulin homology <IMM3>
F;387,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSTCNVTLTCSVEKE---EKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSNN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLILSSVFLFRLFKRRODAASKKTIY 262
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Species: Mus musculus (house mouse)
Jate: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKPP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell surface glycoprotein CD2 precursor - horse
NiAlternate names: T-lymphocyte surface antigen CD2
C.Species: Equus caballus (demestic horse)
C.Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 TILGALERDINLDIPAFOMSEHVEDIQWSKGKTKIAKFKNGS-----MTFQKDKTYEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KNGTLKIKHLERIHEGTYKVDAYDSDGKNVLEETFHLSLLEMVSKPNISW-----
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R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
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8.3%; Score 141.5; DB 2; Length 347;
Best Local Similarity 21.2%; Pred. No. 0.00084;
Matches 63; Conservative 49; Mismatches 136; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 458;
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23.8%; Pred. No. 0.0018;
ative 35; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 23.8<sup>†</sup>
Matches 59; Conservative
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A,Gene: GDB:CD2
A,GCOS-references: GDB:118735, OMIM:186990
A,Map position: 1pl3.1-1pl3.1
A,Map position: 21/1, 128/1, 205/1; 246/1
A,Introns: 21/1, 128/1, 205/1; 246/1
C,Superfamily: T-cell surface glycoprotein CD2
C,Keywords: glycoprotein; T-cell; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-351/Product: T-cell surface glycoprotein CD2 #status predicted <SIG>F;25-206/Domain: extracellular #status predicted <EXT>F;20-234/Domain: transmembrane #status predicted <TMM>F;210-234/Domain: intracellular #status predicted <TMM>F;20-234/Domain: intracellular #status predicted <TMM>F;89,141,150/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.1%; Score 137; DB 1; Length 351; Best Local Similarity 22.6%; Pred. No. 0.002; Matches 73; Conservative 46; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVYSEVQFADKMGKASTQDSKPP 319
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A,Residues: 333-351 <SE3>
R,Seed, B:, Aruffo, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987
A,Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap A,Reference number: A28023, MUD:87204137; PMID:2437578
A,Fitle: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap A,Recession: A28023
A,Molecule type: mRNA
A,Residues: 1-265, Q', ZG7-351 <SEE>
A,Cross-references: GB:M16445; NID:9178668; PIDN:AA451738.1; PID:9178669
A,Cross-references: GB:M16445; NID:9178668; PIDN:AA451738.1; PID:9178669
B,Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; P. A; Reference number: S02292; MUID:87204243; PMID:2883656
A,Reference number: S02292; MUID:87204243; PMID:2883656
A,Reference number: S02292; MUID:87204243; PMID:2883656
A,Rocession: S02292
A,Molecule type: protein
A,Residues: 1-338, "M, 340, QOXTHCPLPLIKKDRNCLFQ' <SA1>
A,Residues: 1-338, "M, 340, QOXTHCPLPLIKKDRNCLFQ' <SA1>
A,Residues: 25-43,132-163
A,Rocession: A30430
A,Rocession: A30430
A,Rocession: A02400
A,Rocession: A02400
A,Rocession: A02400
A,Rocession: A02400
A,Rocession: A02400
A,Rocession: S0229; MUID:89005055; PMID:2901953
A,Reference number: S00829; MUID:89005055; PMID:2901953
A,Molecule type: protein
A,Reference number: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell surface glycoprotein CD2 precursor - human NiAlternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein C; Species: Homo sapiens (man) C; Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 09-Jul-2004 C; Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874 K; Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L. Proc. Nall. Acad. Sci. U.S.A. 85, 1615-1619, 1988 A; Attle: Exon-intron organization and sequence comparison of human and murine T11 (CD2) A; Reference number: A28967; MUID:88144486; PMID:2894031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-351 <DIA>
A,Cross-references: UNIPROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appear r is closely associated with, the erythrocyte receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A;Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.
A;Reference number: A26486; MUID:87041523; PMID:3490670
                                                                                                                                                              412
                                                                                      297
   315 YICEATNPIGTRSGQVEVNITEFPYTPSPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGG 374
                                                                           244 FLFRLFKRRQ----DAASKKTIY--TYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNT
                                                                                                                                                      -- ІРОННРР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 25-46,'X',50 <SE2>
K;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A;Reference number: A28416
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A,Residues: 1-338,'M',340,'QQKTHCPLPLIKKDRNCLFQ' <SE1>
A,Accession: B26486
                                                                                                                                                                                                                          VYSEVQFADKMGKASTQDSK---PPGTSSYE 325
                                                                                                                                                                                                                                                                                              MAQNLQYPD----DSDDEKKAGPLGGSSYE 438
                                                                                                                    375 IVVALRRRRHTFKGDYSTKKHVYGNGYSKAG-
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A,Residues: 1-351 <LAN>
A,Cross-references: EMBL:X07871
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NiAleznate names: CEA; meconium antigen 100
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I53224; I59088; A26
C;Accession: A36319; A27773; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shively, Mol. Cell. Biol. 10, 2738-2748, 1990
A;Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its pron A;Accession: A36319; MUID:90258861; PMID:2342461
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R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: A31037
                                                                                                                                                                                                                                                                                                            72 PVVTVTHRNYYER-IHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYR 130
                                                                                                                                                                                                                                                                                                                                                                                                                      69 AQFRKEKETFKEKDTYKLFKNGTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: | | | | | :: | :: | :: | | | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 VLILSSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVN 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLV-----FYITKRKKQ-----RSRRNDEELETRAHRVATEERGRKPHQIPAS 271
                                                                                                                                                          89
13 LOTWPEAAGKDSEIFTVNGILGESVTFPV-NIQEPRQVKIIAWTSKTSVAYVTPGDSETA
                                                                                                 RLGKPKITQSLMASVNSTC-NVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-----YTCTAQNPVSNNS--DSISARQLCADIAMGFRTHHTGLLSV-----LAMFFLL
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A; Residues: 1-702 <BAR>
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94

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C; Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-termin C; Superfamily: carcinoembryonic antigen, carcinoembryonic antigen, carcinoembryonic antigen, carcinoembryonic antigen precursor amino-terminal homology cCEAN> F; 1.138/Domain: carcinoembryonic antigen precursor amino-terminal homology cCEAN> F; 1.34/Domain: signal sequence #status predicted <SIG> F; 35-678/Product: carcinoembryonic antigen #status predicted <MAT> F; 1.50-217/Domain: immunoglobulin homology <IMM1> F; 25-301/Domain: immunoglobulin homology <IMM1> F; 516-57/Domain: immunoglobulin homology <IMM3> F; 516-57/Domain: immunoglobulin homology <IMM4> F; 608-657/Domain: immunoglobulin homology <IMM5> F; 608-657/Domain: immunoglobulin homology <IMM4> F; 608-657/Domain: immunoglobulin homology <IMM4> F; 609-657/Domain: carboxyl-terminal proneprida #status predicted <F; 679-702/Domain: carboxyl-terminal proneprida #status predicted <F; 679-702/Domain: description for the first of the fi
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C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: S;2048; A31496
K;Kolke, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Tak
EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secrete-A;Reference number: S12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-417 < KOI>
A; Residues: 1-417 < KOI>
A; COSS-references: UNIPROT: PIS151; UNIPROT: Q96BJ1; EMBL: X64116; NID: G35809; PIDN: CAA45
A; Note: G7-Ala was also found
A; Note: the gamma form has 331-Gly and lacks residues 332-384
R; Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
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A; Residues: 1-66, A, 68-417 <MEN>
A; Cross-references: GB:M29535
C; Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
A;Reference number: A90910; MUID:89168426; PMID:2538245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 RRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SP---LGEEGNV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 PELPKPSISSNNSKPVEDKDAVAFTC--EPETQDATYLWWVNNQSLPVSPRLQLSNGNRT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 VTHRNYYERIHALGPNYNLVISDLRMEDAGDY----KAD-INTQADPYTTTKRYNLQIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 PVNIQEPRQVKII------AW-----TSKTSVAYV-----TPGDSETAPVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aymap position: 1993.2-1993.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Reywords: alternative splicing; duplication; glycoprotein; receptor; F;1-20/Domain: signal sequence #status predicted <515</td>

F;1-20/Domain: signal sequence #status predicted content from the figuration of the first specific form of the first specific f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.3%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 LILFNVTRNDTASYKCETQNPVSARRSDSV 229
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24.3%; Pred. No. 0.0
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A; Gene: GDB: PVR; PVS
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;Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105; Reference number: A26831; MUID:87326349; PMID:3632664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: $08106
A;Molecule type: mRNA
A;Molecules: 5-319,321-702 <012>
A;Cross-references: BmBL:X16455; NID:g29854; PIDN:CAA34474.1; PID:g825638
A;Cross-references: BmBL:X16455; NID:g29854; PIDN:CAA34474.1; PID:g825638
A;Barnett, T.
Rubmitted to the EMBL Data Library, September 1991
A;Description: Genomic DNA sequence upstream of the translational start of the carcinoem
A;Accession: S3137
A;Accession: S3137
A;Accession: S3137
A;Accession: S3137
A;Anolecule type: DNA
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R;Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A;Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon A;Reference number: I59098; MUID:87204247; PMID:3033671
A;Accession: I59098
A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 'X', 140-151,'X', 153,'X', 155-156 < THO>
A; Residues: 'X', 140-151,'X', 153,'X', 155-156 < THO>
A; Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer C; Comment: This heavily glycosylated membane protein of unknown function is a widely use C; Comment: This protein may be processed at its C-terminus. It is anchored to the membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-141 <BA2>
A; Cross. 1-141 <BA2>
A; Cross. 1-141 <BABL:X62151
B; Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S. Genomics 14, 384-390, 1992
A; Title: Identification of three new genes and estimation of the size of the carcinoembrange of the size of the carcinoembrange. A; A; Reference number: A44476; MUID:93052339; PMID:1427854
                                  A;Cross-references: GB:M29540; NID:g180222; PIDN:AAA51967.1; PID:g180223
A;Note: the authors translated the codon GTG for residue 130 as Leu
R;Oikawa, S.; Nakazato, H.; Kosaki, G.
Biochem. Biophys. Res. Commun. 142, 511-518, 1987
A;Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA seq
A;Reference number: A25845; MUID:87128144; PMID:3814146
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A;Residues: 35-64 <SIE>
R;Thomas, P.; Toth, C.A.
R;Thomas, P.; Toth, C.A.
A;Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at A;Reference number: A35490; MUID:90321257; PMID:2372297
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Residues: 331-702 <RE2>
Cross-references: GB:M16234; NID:g180240; PIDN:AAA51972.1; PID:g180241
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R;Willcocks, Tcraig, I.W.
Genomics 8, 492-500, 1990
A;Title: Characterization of the genomic organization of human c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Oikawa, S.
submitted to the EMBL Data Library, September 1989
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A, Map position: 19q13.2-19q13.2
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A;Molecule type: DNA
A;Residues: 1-37 <RES>
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A,Molecule type: mRNA
A,Residues: 5-702 <OLK>
A,Cross-references: GB:MI
R;Oikawa, S.
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A;Cross-references: GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51739.1; PID:g178691
R;Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A;Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and indlA;Reference number: A27709; MUID:88268882; PMID:3390172
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A,Residues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-235;
R;Hefta, S.A.; Paxton, R.J.; Shively, J.B.
J. Biol. Chem. 265, 8618-8626, 1990
A,Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci)
A,Reference number: A36271; MUID:90256782; PMID:2341397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194,204-224;233-308;310|
R;Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation A;Reference number: A26414; MUID:87147209; PMID:3469650
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A; Mesdidues: 35-69 cPAX.
R; Riesdidues: 35-69 cPAX.
R; Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
Genomics 14, 384-390, 1992
A; Title: Identification of three new genes and estimation of the size of the carcinoembi
A; Reference number: A44476; MUID: 93052339; PMID: 1427854
A; Accession: E44476
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F.3-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F.35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F.350-301/Domain: immunoglobulin homology <IMM1>
F.321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F.301-344/Domain: carboxyl-terminal propeptide #status predicted <ARN) (covalent F:304)Einding site: carbohydrate (Asn) (covalent) #status predicted F:330/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form
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                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-137, 'L.' 139-344 (BAR>
A; Residues: 1-137, 'L.' 139-344 (BAR>
A) Cross-references: GB:M29541; NID:g189103; PIDN:AAA59915.1; PID:g189104
A; Cross-references: GB:M29541; NID:g189103; PIDN:AA59915.1; PID:g189104
A; Cross-references: GB:M29541; NID:BB:M2040; L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A; Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen
A; Reference number: A29918; MUID:88139389; PMID:2830274
                                                                     NID:g189084; PIDN:AAA59907.1; PID:g189085
othdurft, M.A.; Elting, J.J.
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    A;Residues: 1f238, VV, 240-344 < TAW>
A;Cross-references: GB:M18728; NID:g189084; PIDN:AAAS9907.1; F
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: B31037
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A,Map position: 19q13.2-19q13.2
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A; Residues: 35-141 < KHA>
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A27661

nonspecific cross-reacting antigen precursor - human
NyAlternate names: NCA; TEX/NCA
C; Species: Homo sapiens (man)
C; Date: 31-Mar-1899 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C; Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R; Olkawa. Biophys. Res. Commun. 146, 464-469, 1987
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A; Title: wholecular cloning of agene for a member of carcinoembryonic antigen (CEA) gene A; Reference number: A26902; MUID:8729464; PMID:3619891
A; Accession: A26902
A; Accession: A26902
A; Accession: A26902
A; Accession: A26902
A; Cross-references: UNIFACT: 013774; GB:MI7082; NID:g180230; PIDN:AAA51971.1; PID:g553222
A; Cross-references: UNIFACT: 013774; GB:MI7082; NID:g180230; PIDN:AAA51971.1; PID:g553222
A; Thompson, Ja.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, C
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A; Accession: A29875
A; Molecule type: DNA
A; Reference number: A29875; MUID:87204248; PMID:3033672
A; Note: the authors translated the codon ACT for residue 64 as Tyr
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A; Reference number: A27681; MUID:88106538; PMID:3337731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YTCLFVTFPQGSRSVDİWLRVLAKPQNTAEVQKVQL---TGEPVPMARCVSTGGRPPAQI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 TWHSDLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHESFEKPQLLTVN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 LTVYYPPEVSISGYDNNWYLGQNEATLTCDARSNPEPTGYNWSTTMGPLPPFAVAQGAQL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 LIRPVDKPINTTL----ICNVTNALGARQAELTVQVKEGPPSEHSGMSRNAIIFLVLGI 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 H-----GESGSMAVFHQTQGPSYSESKRLEFVAARLGAELRNASLRMFGLRVEDEGN
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                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                        171;
                                                                         F;344-367/Domain: transmembrane #status predicted <TMN>F;368-417/Domain: intracellular #status predicted <TMT>F;968-417/Domain: intracellular #status predicted <F;49-123,166-221,266-312/Disulfide bonds: #status predicted F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                              DB 1; Length 417;
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159-223/Domain: immunoglobulin homology <IMM2>;259-314/Domain: immunoglobulin homology <IMM3>
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	65; Gaps	STAPVVT		RYNLQIY	ZFHVY	EGNV-	LSNGNMT		
344;		TPGDS	TPGPA	YTTTY	TG		SPRLO		
7.8%; Score 131.5; DB 2; Length 344;	best bocal similarity 23.1%; Flew. NO. 0.003%; Matches 54; Conservative 29; Mismatches 67; Indels	40 PUNIQEPRQUKIIATWTSKTSVAYVTPGDSETAPVVT 75	42 PFNVAEGKEVLLIAHNLPQNRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPA 94	76 VTHRNYYERIHALGPNYNLVISDLRMEDAGDYKAD-INTQADPYTTTKRYNLQIY 129	95YSGRETIYPNASLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQFHVY 141	130 RRIGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEBGNV- 177	142 PELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWVNGQSLPVSPRLQLSNGNWT 199		
DB 2;	67;	SKTSVA	SNSTING	KAD	OVIKSE	TCSVEKEEKNVTYNWSPLGE-	TTYLW	2L 211	7L 234
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                    Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1696
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1: uniprot_sprot:*
2: uniprot_trembl:*

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UniProt

Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SUMMARIES

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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
25-OCT-2004 (TrEMBLrell. 28, Last annotation update)
Leukocyte antigen CD84 (Leukocyte differentiation antigen CD84 isoform
CD84c) (MAX.3 cell surface antigen precursor) (CD84 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20164057; PubMed=10698700; DOI=10.1042/0264-6021:3460729; Krause S.W., Rehli M., Heinz S., Ebner R., Andreesen R.; "Characterization of MAX.3 antigen, a glycoprotein expressed on mature macrophages, dendritic cells and blood platelets: identity with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hafeh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bloak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86188202; PubMed=3008886; And Emmrich F.; Andressen R., Bross K.J., Osterholz J., Emmrich F.; Human macrophage maturation and heterogeneity: analysis with a newly generated set of monoclonal antibodies to differentiation antigens.";
                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILINE=97454416; PubMed=9310491;
MEDILINE=97454416; PubMed=9310491;
de la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
"CD84 leukccyte antigen is a new member of the Ig superfamily.";
Blood 90:2398-2405(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Lymph;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palou E., Sole J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                        328 AA.
ALIGNMENTS
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Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Koriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                           Query Match 99.9%; Score 1695; DB 2; Length 328; Best Local Similarity 100.0%; Pred. No. 3.2e-125; Matches 328; Conservative 0; Mismatches 0; Indels
                                                                                                                 MAX.3 cell surface antigen.; 6C9A89206A6D0344 CRC64;
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328 AA; 36871 MW;
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SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Name=CD84;
Homo sapiens (Human).
                                                                                                 SEQUENCE FROM N.A.
                                                                                                            rissue=Lymph;
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                                                                                                                                                                                                                                                                                                                                                  Gaps

    21 Potential.
    22 339 leukocyte differentiation antigen CD84.
    339 AA; 38082 MW; B78D6D5CAC8D3604 CRC64;

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Catarrhini, Hominidae, Homo.
Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J.; Submitted (UUr.2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR541847; CAG46645.1; -..
InterPro; IPR00110; Ig-11ke.
SMART; SM00409; IG; 2.
PROSITE; PSS00835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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                                                                                                                                                                                                                                                                                                   Length 328;
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Best Local Similarity 96.5%; Pred. No. 2e-123;
Matches 327; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                  Indels
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y12632; CAA73181.1; -.
SWART; SM00409; IG; 1.
                                                                                                                                                                                                                                                 328 AA; 36861 MW; 6C9A8BDD45BD0344 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 precursor.
                                                                                                                                                                                                                                                                                              Query Match
99.5%; Score 1687; DB 2;
Best Local Similarity 99.7%; Pred. No. 1.4e-124;
Matches 327; Conservative 0; Mismatches 1;
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Mammalia; Eutheria; Primates;
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61 AYVIPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 120
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Palou E., Freed J.H., Sole J., Pi A., Vilella A., Vives J., Gaya A.;
Palou E., Freed J.H., Sole J., Pi A., Vilella A., Vives J., Gaya A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U96627, AAD04232.1;
InterPro, IPR003599; Ig.
InterPro, IPR00710; Ig-like.
EMART; SM00409; IG; 1.
PROSITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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QSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKPPGTSSYEIVI 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palou E., Sole J., Pirotto F., Gaya A.;
Palou E., Sole J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF054817, AAR21723.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
SMART; SM00409; IG, 1.
PROSITE; PS0835; IG LIKE; 1.
SEQUENCE 272 AA; 30514 WW; 6A2E13AA4E22E13E CRC64;
                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD84d.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                  Name=CD84;
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                                   AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                                                    61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054816; AAF21722.1; -
Genew; HGNC:1704; CD84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPRO03599; IG.
INTERPRO; IPRO07110; IG-like.
SMART; SM00409; IG; 1.
PROSTIE: PSS0835; IG LIKE; 1.
SEQUENCE 345 AA; 38782 MW; DA06BC5A682E62DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
Leukocyre differentiation antigen CD84 isoform CD84a.
Name=CD84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEEPVNTVYSEVQFADKAGKASTQDSKPPGTSSYEIVI 328
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Best Local Similarity 94.8
Matches 327; Conservative
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Name=CD84;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
                                                                                                                                                                                                                                                                                  61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYRADINTQADPYTT 120
                                                                                                                                                                                                                                                                                                                                                                                                      121 TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI 180
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                                                                                                                                                                              1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 FOTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AYVIPGDSETAPVVIVIHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTI
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                                                                                                                                                 1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                                                                                                                  61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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66.3%; Score 1125; DB 2; Length 241;
Best Local Similarity 94.3%; Pred. No. 1.7e-80;
Matches 215; Conservative 2; Mismatches 5; Indels
                                                  Length 280;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Palou B., Sole J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF054818; AAF21724.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
SMART; SM00409; IG; I.
SEQUENCE 241 AA; Z6902 MW; F0121BC1609B6C52 CRC64;
31651 MW; A043E048E762A718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD848:
                                               77.8%; Score 1320; DB 2; 100.0%; Pred. No. 8.9e-96;
                                                               100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 SSVFLFRLFKRRQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSVFLFRLFKRRQ 253
                                                                                              Matches 253; Conservative
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280 AA;
                                               Query Match
Best Local Similarity
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SEQUENCE
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77 THRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPK 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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MEDLINE=20208572; PubMed=10746783;
Palou E., Pirotto F., Sole J., Freed J.H., Peral B., Vilardell C.,
Vilella R., Vives J., Gaya A.;
"Genomic characterization of CD84 reveals the existence of five
"solorms differing in their cytoplasmic domains.";
Tissue Antigens 55:1181-127(2000).
EMBL; AF101031; AAF06840.1; --
EMBL; AF101030; AAF06840.1; JOINED.
                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sciurognathi, Muridae, Murinae, Mus
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TISSUE=Peritoneum;
MEDLINE=99180614; Pubmed=10079287; DOI=10.1007/s002510050490;
de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 197;
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197 AA; 21889 MW; 2E660BF5FAB71D88 CRC64;
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Last annotation update)
                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte antigen CD84 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.7%; Score 1029; DB 2;
100.0%; Pred. No. 4.8e-73;
ive 0; Mismatches 0;
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197 AA
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003599; IG.
Interpro; IPR007110; IG-like.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD84 leukocyte antigen.
Name=Cd84; Synonyms=CD84;
Mus musculus (Mouse).
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PRELIMINARY;
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tes 197; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 FOTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSVFLFRLFKRRQDA-----ASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 99-655 FROM N.A. (ISOFORM 3).
Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20424510; PubMed=10970033; DOI=10.1007/s002510000209;
MEDLINE=20424510; PubMed=10970033; DOI=10.1007/s002510000209;
Tovar V., de la Puente M.A., Pizcueta P., Bosch J., Engel P.;
Tovar V., de la Fuente E personale leukocyte cell surface molecule Ly9.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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Q9HBG7; Q14775; Q9H4N5; Q9NQ24;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen (Cell-surface molecule Ly-9) (CD229 antigen).
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Sandrin M.S., Henning M.M., Lo M.F., Baker E., Sutherland G.R.,
McKenzie I.F.;
                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                              Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                       Indels
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                  43BB1AA5AF1989E0 CRC64;
                                                                                                                                                                                                                                                                        55.7%; Score 944.5; DB 2;
larity 57.3%; Pred. No. 4.1e-66;
Conservative 48; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVNTVYSEVQFADKMGKASTQDSKPPGTSSYEIVI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 PVTTIYSSVQLSEKMKETNMKDRSLPKALGNEIVV 329
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SEQUENCE OF 32-654 FROM N.A. (ISOFORM 2).
Immunogenetics 49:249-255(1999).
EMBL; AF043445; AAD02273.1; -.
MGD; MGI:1336885; Cd84.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
SWART; SW00409; IG; 1.
SROSITE; PS50835; IG LIKE; 1.
SEQUENCE 329 AA; $7345 MW; 43B
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Immunogenetics 43:13-19(1996).
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                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 192; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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GO; GO:005887; C:integral to plasma membrane; ISS.
GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); NAS.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
                                                                                                                                                                                                         SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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                                                                                                Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-lymphocyte surface antigen Ly-9. Extracellular (Potential). Potential.
Pfam; PF00047; ig; 2. SMART; SM00409; IG; 2. SMART; SM00409; IG; 2. SMART; SM010409; IG; 2. ARGSIF, IG_LIKE; 2. Alternative splicing; Antigen; Cell adhesion; Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (In Ref. 1).
V -> M (in Ref. 4).
9FB0A3056D79F80A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal, Transmembrane.
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(GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
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Ig-like C2-type 1.
Ig-like C2-type 2.
Ig-like C2-type 2.
Potential.
Potential.
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                                                                                     Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GlcNAc.
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                                                                                                                                                                               IsoId=Q9HBG7-2; Sequence=VSP_002525;
                                                                                                                                    Name=1;
IsoId=Q9HBG7-1; Sequence=Displayed;
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EMBL; L42621; AAA92633.1; -.
EMBL; AL121985; CAC00580.1; -.
EMBL; AY007142; AAG02002.1; -.
Genew; HGNC:6730; LY9.
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                                                                                                                                      89 FARPKEN-----VTIMVKSYLGRLDITKWSYSLCISNLTLNDAGSYKAQINQRNFEVTTE 143
                                                                                                                                                                   122 KRYNLQIYRRLGKPKIT-QSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEE 174
                                                                                                                                                                                   144 EEFTLFVYEQLQEPQVTWKSVKVSENPSCNITLMCSVKGAEKSVLYSWTPREPHASESNG 203
                                                                                                                                                                                                                          175 GNVLQIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLA 231
                                                                       232 MFFLLVLILSS-----VFLFR---LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
                                                                                                                                                                                                                                                                                                  263 BPVTLPLALPACRDTEKVVWLFNTSIISKERBERAATADPLI-----KSRDPYKNRVW 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CS7BL/6J; TISSUE-Aorta and vein, and Thymus; MEDLIRE=20499374; DubMed=110421159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Shibata K., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res: 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                       3 QHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUB=Aorta and vein, and Thymus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki P., Carninci P., Hayashizaki Carning.";
                             Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 16 days neonate thomso CDNA, RIKEN full-length enriched library, clone.Al30013D2 product: CDN4 antigen, full insert sequence (Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone.AS30016Al3 product: CD84 antigen, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                          37;
  Length 655;
                           Indels
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; Score 382.5; DB 1;
; Pred. No. 1.7e-21;
60; Mismatches 100;
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Query Match
Best Local Similarity 33.9
Matches 101; Conservative
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A Adachi C. Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hangaki T., Haraka T., Bono H., Carninci P., Fukuda S., Furuno M., Hangaki T., Haraka T., Hirozane T., Horari P., Imotani K., Hayatiu N., Hiramoto K., Hiracka T., Hirozane T., A Hori P., Imotani K., Ishii Y., Kondo S., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matuyama T., Miyazaki A., Murata M., Nakamura M., A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sakai C., Sakai K., Shihara K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T., Sumitted (UJUL-2001) to the EMBL/GenBank/DDBJ databases.

R. EMBL, AK007385; BAC20799:1; -.
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=110.7 Kateunai T., Tashiro H., Itoh M., Sumi N., Ishlin Y., Nakamura S., Hazama M., Mishine T., Harada A., Aumamoto R., Matsuncto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Tanaka T., Ohara E., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Nakaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system=384-format sequencer.";

Genome Res. 10:1757-1771(2000).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F., Blatchenco L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L., Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Ra Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H., A Hilalon D.K., Muzny D.M., Sodergran B.J., Lu X., Gibbs R.A., A Villalon D.K., Muzny D.M., Sodergran B.J., Lu X., Gibbs R.A., Antialon D.K., Muzny D.M., Sodergran B.J., Lu X., Gibbs R.A., Antialon D.K., Muzny D.M., Schern B.J., Lu X., Gibbs R.A., Antialon M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Antesley M., Schelmuz J.D., Nyers R.M., Butterfield Y.S., A Rodriguez A.C., Grimwood J., Schmuzz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., The M., Shalsk W., Shalsk W., Shalsk W., Tand mouse cDNA sequences.", The mouse cDNA sequences.", The proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LWSLLLLLQEAKGFSGDDEDPEEVIGVLQESINLSLEIPSNEEIKHIDWLFQNNIAIVKP
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.2%; Score 376; DB 2; Length 285; 34.3%; Pred. No. 2e-21; ive 45; Mismatches 129; Indels
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Zhang W., Wan T., Li N., He L., Yuan Z., Yu M., Cao X.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019477; AAH19477.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1923692; Slamf9.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
SMART: SMO409; IG; 1.
PROSITE; PSS0835; IG LIKE; 1.
SEQUENCE 285 AA; 31728 MW; D84BFF8142367F81 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 28, Last annotation update)
CD84-H1 (CD2 family 10) (SLAM family member 9).
Name-SLAMF9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 34.38 Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Q96A28
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TISSUEDCE FROM N.A.

TISSUES PROJUED tissue;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeberg B. A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeberg B. Buerow K.H., Schamen C.M., Schuler G.D.,

Altschul S.F., Zeberg B. B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Attachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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[2]
SEQUENCE FROM N.A.
MEDLINE=21541411; Pubmed=11685473; DOI=10.1007/8002510100364;
Fennelly J.A., Tiwari B., Davis S.J., Evans B.J.;
"CD2F-10: a new member of the CD2 subset of the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.0%; Score 373; DB 2; Length 289; 32.1%; Pred. No. 3.6e-21; ive 54; Mismatches 119; Indels
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SEQUENCE 289 AA; 32436 MW; 2FB67EE8B4D18205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                  [mmunogenetics 53:599-602(2001).
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InterPro; IPR007110; Ig-like.
SMART; SM00409; IG; 1.
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EMBL; AY034613; AAK61389.1;
EMBL; BC074754; AAH74754.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
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92; Conservative
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Submitted (JUN-2004)
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A Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Alzawa K., Akimura T., Hara A., Habhizume W.,

A Hayabhida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksato N.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tomaru A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Lu Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIŜSUE=B lymphocyte;
MEDLLNE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLLNE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                        TISSUE=B lymphocyte;
MEDLYNE=9927923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
MEDLYNE=99279223; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus B lymphocyte B cells CRL-1702 WEHI 231 cDNA, RIKEN full-
length enriched library, clone:G430073H03 product:weakly similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=B lymphocyte;
MEDLINE=2050913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-flormat
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                      IISSUE=B lymphocyte;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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   282
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 PRELIMINARY;
                                                                                                             CD84-H1 (CD2 FAMILY 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=B lymphocyte;
The FANTOM Consortium,
                                                                                                                                             (Mouse)
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                               musculus
                                                                                                                              Name=Slamf9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SPLGEEGNVLQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 IFQTPEDQELTYTCTAQNPVSN-NSDSISARQLCADIAMGFRTHHTGL-LSVLAMFFLLV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 TSWRPGDKAPSYTCRVSNPVSNISSHRISVGSFCAD--PGYPEKPSMLCLLVKSLFLLLL 242
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS7BL/61; IISSUE=Tongue;
The FANTOM COMBORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                        6 LWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTP
                                                                                                                                                                                                                                                                                                                                                                                                                             LWSLLLLLQEAKGFSGDDEDPEEVIGVLQESINLSLEIPSNEEIKHIDWLFQNNIAIVKP
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                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue CDNA, RIKEN full-length enriched
library, clone:2310026104 product:weakly similar to CD84-H1 (CD)
                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                           Score 368; DB 2; Length 28
Pred. No. 8.7e-21;
9; Mismatches 111; Indels
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SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Tongue;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
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MGD; MGI:1923692; Slamf9.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
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36.5%; Pre
tive 39;
                                                                                                                                          SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 285 AA; 31759 MW;
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LAILTVGLCLFRAQK 257
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Job time : 147.561 secs
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SEQUENCE KNOW N.A.

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Pukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Pukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konom H., Kowda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Tejima Y., Toya T., Yaammura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
A Tejima Y., Toya T., Yaammura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Rubited (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK009505; BAB26328:1; -.
R GO; GO:0016615; C::extracellular space; TAS.
R GO; GO:0016621; C:integral to membrane; TAS.
R InterPro; IPR003599; IG.
R InterPro; IPR003599; IG.
R InterPro; IPR003599; IG.
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    STRAIN=CS7BEL/6J; TISSUE=Tongue; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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35.2%; Pred. No. 1e-20;
ive 42; Mismatches 117; Indels 12; Gaps
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Shibate K., Itoh M., Aizawa K., Nagacka S., Sasaki N., Carninci P., Skonno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M., Sumi N., Ishii K., Katsunai T., Tashiro H., Itoh M., Yamamoco R., Matsunaco S., Hazama M., Nishine T., Harada A., Yamamoco R., Matsunaco H., Sakaguchi S., Ikegami T., Rabilwagi K., Fujiwake S., Inoue K., Togawa M., Ohara B., Matahiki M., Ohaca Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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SEQUENCE 285 AA; 31764 MW; 33BDB4A633A5C1B3 CRC64;
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LAILTVGLCLFRAQKSYETPRVRK 266
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Matches 93; Conservative
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Search completed: February 4, 2005, 12:15:00

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AJ22334 Homo sapi
CR541847 Homo sapi
AF054816 Homo sapi
AF054817 Homo sapi
AF054818 Homo sapi
AF054818 Homo sapi
AF07345 Mus muscu
AF101030 Homo sapi
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AX474332 Sequence
AX474333 Sequence
AX474241 Sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
AX924719 Sequence
BC020063 Homo sapi
CQ718714 Sequence
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 29 from Patent EP1223218.
AX474268
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HSU96627
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AF043445
HSLDA1
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BCC74754
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AX275725
AY324613
AX357479
HSA306388
AX574548
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AL35596
AC012471
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99.9 3173
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98.6 1110
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66.3 1239
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35.8 175386
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Best Local Similarity:
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DEFINITION
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JOURNAL
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AUTHORS
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AX474268
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    Score:
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-Q=/cgn2_1/USPTO spool/US09882171/runat_04022005_114004_26025/app_query.fasta_1.910
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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U82988 Human leuko
AF054815 Homo sapi
BD191209 186 human
                                                                                             February 5, 2005, 03:24:06; Search time 5771.83 Seconds (without alignments) 2761.994 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                     nucleic search, using frame_plus_p2n model
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/ Gene="CD84" / Godon_start=1 / Codon_start=1 / CD84c" CD84c" / CD84c"	Alignment Scores: 7.03e-158 Length: 1067 Pred. No.: 1695.00 Matches: 328 Score: 328 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 99.94% Indels: 0 DB: 99.94% Caps: 0		190		MetGlukspalaglykspfyrlysalaaspfleasnfhrglnalaaspfofyrfhrfhr 	121 The Lyang Tyrasoleu Gloule Fyrargaseleu Glytos Frologial Enfrance 140
Oy 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120 342 ATGGAAGACGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 401 342 ATGGAAGACGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 401 Qy 121 ThrLySARGTYRASNLeuGlnIleTyrArgArgLeuGlyLy8ProLy8IleThrGlnSer 140 402 ACCAAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGT 461 Qy 141 LeuwetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160 161 [221 702 241	762 TCTTCAGTGTTTTTGTTCCGTTTGTTCAGAGAGACAAGATGCTGCCTCAAGAAAAACCC 261 IleTyrThrTyr1leMetAlaSerArgAsnThrGlnProAlaGluSerArg1leTyrAsp	Qy 281 GlulleLeuGInSerLysValLeuEroSerLysGluCluProValTyTA31TyTSer 300 Db 882 GAAATCCTCCAGGCTCCTTCCTCTCCAGGAAGAGCCAGTGAACACAGTTTATTCC 941 Db 301 GluValGInPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly 320 Cl 1	Oy 321 ThrserSerTyrGlulleVallle 328 	AF054815 LOCUS AF054815 LOCUS Homo sapiens leukocyte differentiation antigen CD84 isoform CD84c CCBSION AF054815 AF054815 AF054815.1 GI:6650105 KEYWORDS KEYWORDS SOURCE Homo sapiens (human) ONGANISM Homo sapiens (human) AUTHORS BURATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Direct Submission JOURNAL JOURNAL LOCATION Barcelona 08036, Spain FEATURE LOCATION ALTOP Barcelona 08036, Spain LOCATION VILLAR HOMO Sapiens LOCATION ALTOP Barcelona 08036, Spain LOCATION ALTOP Barcelona 08036, Spain LOCATION ALTOP BARCELONAR-1998 AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AGENETICATION ALTOP BARCELONAR-1998 AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AGENETICATION ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA" AMD ARTERIANA AMD ARTERIANA AMD ARTERIANA AMD ARTERIANA AMD ARTERIANA AMD ARTERIANA AMD ARTERIANA AMD ARTERIANA AMD AMD ARTERIANA AMD AMD ARTERIANA AMD ARTERIANA AMD AMD ARTERIANA AMD AMD ARTERIANA AMD AMD ARTERIANA AMD ARTERIANA AMD AMD ARTERIANA AMD AMD ARTERIANA AMD AMD ARTERIANA AMD AMD AMD AMD AMD AMD ARTERIANA AMD AMD AMD AMD AMD AMD AMD AMD AMD AM

Score: 1695.00 Matches: 328 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 99.94\$ Indels: 0 DB: 6 Gaps: 0 US-09-882-171-483 (1-329) x BD191209 (1-3173) Qy 1 MetAlaGlnHisHisLeuTrpTleLeuLeuLeuCyștLeuGlnThrTrpProGluAlaAla 20		Qy 41 ValAsnIleGInGluProArgGInValLysIleIleAlaTrpThrSerIysThrSerIval 60 Db 171 GTAAATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATTGTT 230 Qy 61 AlaTyrValThrProGlyAspSerGluThrAlaProValThrHisArgAsn 80 Ch 61 AlaTyrValThrProGlyAspSerGluThrAlaProValThrHisArgAsn 80	1 TyrTycluarglleHisalaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArg 10	121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 14		651 AACAAITCTGACTCCTGCCCGGCAGCTCTGTCCAGACATCGCAATGGGGTTTCCGT 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu 111 ACTCACCACCAGGGTTGCTGTGTTTTTTTTTTTTTTTTT	Qy 261 IleTyThrTyrileMetAlaSerArgasnThrGlnBroAlaGluSerArg11eTyrksp 280
Qy 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysLysLysThr 260 Db 790 TCTTCAGTGTTTTTGTTCCGTTTGTTCAAGAAAGAAGAAGAAGAAGAAAACC 849 Qy 261 IleTyrThrTYTIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280 Bb 850 ATATACACATATATCATGGCTTCAAGGAACACCCAGCCAG		Qy 321 ThrSerSerTyrGlulleValIle 328	1 186 human secreted proteins. BD191209 BD191209.1 GI:33000948 JP 2002510192-A/173. unidentified unclassified 1 (bases 1 to 3173)	4	COMMENT PN JP 2002510192-A/173 PD 02-ARR-1998 JP 1998538883 PF 06-MAR-1997 US 60/040162,07-MAR-1997 US 60/040333 PR 07-MAR-1997 US 60/040161 PR 07-MAR-1997 US 60/040626,07-MAR-1997 US 60/040334 PR 07-MAR-1997 US 60/040334 PR 07-MAR-1997 US 60/040336,07-MAR-1997 US 60/040336,07-MAR-1997 US 60/040336,07-MAR-1997 US 60/040336,11-APR-1997 US 60/043568 PI STEVEN M RUBEN CRAIG A ROSEN,CARRIE L FISCHER,DANIEL R SOPPET, PI KENNETH C CARTER,DANIEL P BEDNARIK,GREGORY A ENDRESS,GUO LIANG	PI YOU, JIAN NI, PI YOU, JIAN NI, PI PING FENG, PAUL E YOUNG, JOHN M GREENE, ANN M FERRIE, ROXANNE DUAN, PI JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S OLSEN, REINHARD EBNER, PI LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI YI LI, ZHIZHEN ZENG, PI HLA KYAW PC CLANIS/10, C12N1/21, C07K14/47, C07K16/18, C12Q1/68, PC G01N33/50,	C GINN33/S3,GOIN33/68,A6IK38/17 CC Strandedness: Double; CC Topology: Linear; FH Key Location/Qualifiers. FEATURES Location/Qualifiers. FEATURES Location/Qualifiers. Location/Qualifiers. Location/Qual

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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bhat, N.K.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Morkernan, K.J., Mallak, S.J., Boask, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Walk, N., Sodergren, E.J., Lux, Gabbe, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Kohrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butkesley, R.W., Touchman, J.W., Green, E.D.,
Butkerfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse obna sequence of the sequence of
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Homo sapiens CD84 antigen (leukocyte antigen), mRNA (cDNA clone
MGC:21324 IMAGE:4385965), complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
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                                       ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu
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1186 human scretch proteins
Patent: EP 1352962-A 174 15-OCT-2003;
HUMAN GENOME SCIENCE, INC. (US)
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Sequence 174 from Patent EP1352962.
AX924719
AX924719.1 GI:40242664
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                                                                                             GCTTATGTAACACCCAGGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCCACAGAAAT
                                                                                                                                               TyrTyrGluArg11eHisAlaLeuG1yProAsnTyrAsnLeuVal11eSerAspLeuArg
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                                                                                                                                                                      TATTATGAACGGATACATGCCTTAGGTCCCGAACTACAATCTGGTCATTAGCGATCTGAGG
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RIYDEILQSKVLPSKEEPVNTVYSEVQFADKMCKASTQDSKPPGTSSYEIVI"
                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 26 Row: o Column: 19
This clone was selected foor full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502686. Location/Qualifiers

1. 3278
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                                                                          Contact: MGC help desk
Email: cgapbe-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center.
Sequencing Center.
Sequencing Center.
Conter: am@@bcm.tmc.edu
Contact: am@@bcm.tmc.edu
Contact: am@@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
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A.N., Gibbs, R.A.
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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                                                                                                                                                          Krause, S.W., Rehli, M., Heinz, S., Ebner, R. and Andreesen, R. Characterization of MAX.3 antigen, a glycoprotein expressed on mature macrophages, dendritic cells and blood platelets: identity
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xrause, S.W.
Direct Submission
Submitted (05-FEB-1998) Krause S.W., Hematology, University of Regensburg, Franz Josef Strauss Allee 11, Regensburg, D 93042, GERMANY
              GlulleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer
                                                                                      GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly
IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp
                                                                                                                                                                                                                                                                                                                                                                                    cell surface antigen; glycoprotein; MAX.3 antigen.
Homo sapiens (human)
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Homo sapiens mRNA for MAX.3 cell surface antigen.
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108. .1028
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20164057
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Patent: WO 02068579-A 4648 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
1. 3296
/ Organism="Homo sapiens"
/ mol_type="unassigned DNA"
/ db_xref="taxon:9606"
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This clone is available from RZPD,

Contact RZPD (customer.service@rzpd.de) for further information.

This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of

Proteomics (HIP) and RZPD.

This CDS has been cloned without stopcodon.

The CDS has been cloned without stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase(TM)

reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GCA CAC (ATC).

The last codon is followed by the 3' att site: GACCCAGCTTTCT. att

The clone is validated by full sequence check.

Compared to the reference sequence NM 003874 (GI:4502686) we found

AA exchange(8) at position (first base of changed triplet):

BB0 (pro--ser)
CR541847 1994 pp mRNA linear PRI 29-JUN-2004 Homo sapiens full open reading frame CDNA clone RZPDo834H0132D for gene CD84, CD84 antigen (leukocyte antigen); complete cds, without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Germany
TSPD; RZPD0834H0132D, ORFNO 3790
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H0132D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB NO.
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 994)
Halleck, A. Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J. Cloning of human full open reading frames in Gateway (TM) system entry vector (pDONR201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total to 984)
Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S.,
Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 110
www.rzpd.de
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/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="REXDOS84#01320"
/clone lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5Alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
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                                                                ThrSerSerTyrGluileValile 328
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Full ORF shuttle clone,
Homo sapiens (human)
Homo sapiens
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/gene="CD84"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Direct Submission
Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Submitted(15-APR-1997) A. Gaya, Hospital Clinic, Servei
Immunologia, Villarroel 170, Barcelona 08036, SPAIN
Location/Qualifiers
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AF054816 1118 bp mRNA linear PRI 01-JAN-2000 Homo sapiens leukocyte differentiation antigen CD84 isoform CD84a (CD84) mRNA, complete cds.

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                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1118)
Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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/product="leukocyte differentiation antigen CD84 isoform
CD84a"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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SM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 967)

RS Palou, E., Sole,J., Pirotto,F. and Gaya,A.

Direct Submission

AL Submission

AL Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic,

Villarroel 170, Barcelona 08036, Spain

Location/Qualifiers

1. 967

| Organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                           AF054817

Homo sapiens leukocyte differentiation antigen CD84 isoform CD84d (CD84) mRNA, complete cds.

AF054817.1 GI:6650109
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70. 888
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CD84d"
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                                                                                                                                                 TCCTGCTTGAACACCTTCACTAAGAACCCTTATGCTGCTCAAGAAAACATATAACACA
                                                                                                                                                                                                                TyrileMetAlaSerArgAsnThrGlnProAlaGluSerArgileTyrAspGluIleLeu
                                                                                                                                                                                                                          TATATCATGGCTTCAAGGAACACCCAGCCAGCAGAGTCCAGAATCTATGATGATGAAATCCTG
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                                                                                     AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg
                                                                                                                    ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu
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1. _967
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AF054817
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240 220 789 260 369 120 429 ThriysargTyrasnLeuGlnIleTyrargArgLeuGlyLysProLysIleThrGlnSer 140 489 160 549 180 609 200 699 729 249 100 40 9 80 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArglleTyrAsp AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer rcricagigiririgirccgrrrgrrcaagagaa-----967 294 1 0 34 Length: Matches: Conservative: Mismatches: Indels: Gape: (1-967)

140

489 160 549

369 120 429

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isoform CD84s
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 888)
Palou,E., Sole,J., Pirotto,F. and Gaya,A.
Direct Submission
Submitsed (20-MAR-1998) Servei d'Immunologia, Hospital Clinic,
Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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250 GCTIATGIAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAAT
                         TyrTyrGluhrglleHisAlaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArg
                                      AF054818

Homo sapiens leukocyte differentiation antigen CD84 (CD84) mRNA, complete cds.
AF054818
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70. .795
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Homo sapiens CD84 mRNA, alternatively spliced, complete cds.
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U96627.1 GI:4100318
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Palou,E., Freed,J.H., Sole,J., Pi,A., Vilella,A., Vives,J. and
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                                                                                  rgluvalginphealaaspiysmetgiyiysalaserThrginaspseriysProProgi
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Submitted (07-APR-1997) Servei Immunologia, Hospital Clinic,
Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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GGAAAAGATGCAGACCCGGTGGTAATGAATGGGATTCTTGGGGAGTCAGTTACTTTCCTC 174
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                                      Molecular cloning, characterization, and chromosomal localization of the mouse homologue of CD84, a member of the CD2 family of cell
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Bosch, J. and
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GCTTTTATAAAACCAGGAGTCAATAAAGCTGAA-----GTTACCATAACCAGGGCACT
                                                                                                                                                             Gases 1 to 1132)
de la Fuente, M.A., Tovar, V., Pizcueta, P. and Engel, P.
Direct Submission
Submitted (17-JAN-1998) Immunology Unit, Department of Cellular
Biology, Medical School, University of Barcelona, Casanova 143,
Barcelona 08036, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetalaGlnHisHisLeuTrplleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla
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de la Fuente, M.A., Tovar, V., Pizcueta, P., Nadal, M.,
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Matches:
Conservative:
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Immunogenetics 49 (4), 249-255 (1999)
99180614
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Mus musculus CD84 leukocyte antigen (CD84) mRNA, complete cds.
AF043445 AF04345-1 GI:4105142
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria;
1 (bases 1 to 1132)
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           406 ACCAAGATCTACCTTCATATCTACCGTCGACTTAAAACACCAAAAATTACACAGAGT 465
                       201 AsnasnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
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SUMMARIES

Aab47878 SCZ/CD84 Description Ade26238 Ad18297 Ad19067 Adq19067 Adw74891 Aww74891 Aww74891 Adw233198 Ad157243 Ad157243 Ad157243 Ad157243 Ad157243 Ad157103 Ad157243 Ad157103 Ad157243 Ad157103 Ad26244 Aww01829 Aww01829 Aww01829 Aww01829 Aww01829 Aww01829 Abw01829 Abw01829 Abw01829 Abw01829 AAE26238 ADC05708 ADC05708 ADP23943 AAW74891 ABG95343 ABG95343 ABG953138 ADI23198 ADI23198 ADL57243 ADL57105 ABG96270 ADK98560 AAB47878 OB Length Query Match 1000.0 10 Score Result No.

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AAE26246 ABW01826 AAE26249 ABW01829 AAE26244

ALIGNMENTS	RESULT 1 AAB47878 LD AAB47878 standard; protein; 328 AA.	AX AC AAB47878;	AA DT 02-MAY-2002 (first entry)	AA. DE SCZ/CD84.	A. SCZ; CD84; platelet; monocyte; circulating B cell; schizophrenia; allele; KW polymorphic marker; chromosome 1q22.	XX OS Homo sapiens.	AA PN WO2002024-A2.	XX PD 10-JAN-2002.	AA PF 23-APR-2001; 2001WO-US013040.	XX PR 21-APR-2000; 2000US-0198873P.	XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.	XX PI Brzustowicz LM, Bassett AS;	AX WPI; 2002-171605/22. DR N-P5DB; AAI72383.	XX prognosing susceptibility to schizophrenia (SCZ) in a patient, by PT determining presence or absence of an allele of a linked polymorphic PT marker present on chromosome 1q22, were the marker is linked to a variant PT form of the SCZ gene.	XX PS Example 6; Page 70; 82pp; English.	This sequence is encoded by the SCZ gene which was isolamethod of the invention. The SCZ gene has been previousl CD84, GenBank Accession No: NM 001874. CD84 is a 73 kDa on platelets, monocytes and circulating B cells. This pinvolved in the processes by which the brain responds to stimuli, Therefore they may provide targets for theraper stimuli. The SCZ sequence may	method of diagnosing susceptibility to schi method comprises determining the presence of linked polymorphic marker in the DNA of the marker is present in chromosome 1q22 and is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, usefu
for treating immune, inflammatory, or hepatic circulatory disorders.
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                                                                                                                                                                          KDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
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                                                                                                       Gaps
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                                                                    Length 328;
a variant form associated with a phenotype of schizophrenia
                                                                                                       Indels
                                                                  100.0%; Score 1039; DB 5;
100.0%; Pred. No. 6.7e-88;
ive 0; Mismatches 0;
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                                                                                                         Conservative
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nes 199; Conserv
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                                     Sequence 328 AA;
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and SLAM associated protein (SAP) motifs. CD2000 DNA and protein is useful for treating disorder such as immune proliferative disorders, immune disorders (e.g. carcinoma), viral infection, autolmmune disorders (e.g., arthritis, multiple scolerosis, Garave's disease, and Hashimoto's disease), T cell disorder (e.g. acquired immune deficiency syndrome (AIDS)), inflammatory disorders (e.g. crohn's disease and ulcerative (colitis), inflammatory disorders (e.g. theumatory syndrome orteoarthritis), apoptotic disorders (e.g. systemic lupus erythematosus, and psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytocoxic disorders, septic shock, cronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical thrappeutic and phramacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD84 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTSVAYVTPGDSETAPVVTVHRNY
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schoenfeld JR,
                                                                                                                                                                                                                                                                                                                                                                                               9; DB 5;
6.7e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene Therapy; PRO; B cell related disorder; immune-mediated inflammatory disease; human.
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1039;
100.0%; Pred. No. 6.7
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dennis K, Fong S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL82907 standard; protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSDSISARQLCADIAMGFR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-2003; 2003WO-US029097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-2002; 2002US-0411392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO24934, SEQ ID 109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark H,
                                                                                                                                                                                                                                                                                                                                                                   Sequence 328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004024097-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL82907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL82907
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The invention relates to treating a subject having a condition that benefits from modulating the balance of regulatory T cell function call function.

CC chaive to effector T cell function, or vice versa, in a subject. The method involves administering an agent that modulates the expression or activity of a molecule selected from PTGER2 and TGFbetal, or Jagged-1, CG PRR-12, CD89, SCD89, serotonin R, BY55, serotonin R2C, GPR63, CC histamine R-H4, GPR58, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, DBE-4d, and PI-CG are useful for diagnosing, preventing or treatment occurs. The methods are useful for diagnosing, preventing or treating conditions call activity of call response to antigens associated with the condition, such as in an call response, an autoimmune disorder, a viral infection, a microbial infection, a parasitic infection a tumour. The present sequence represents a human leukocyte differentiation CD84 antigen, preferentially expressed in regulatory T cells.
                                                                                                                                                                                                                                                                                   Treating a condition that benefits from modulating regulatory or effector T cell function comprises administering an agent that modulates the expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbetal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1039; DB 8; Length 328; 100.0%; Pred. No. 6.7e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human soft tissue sarcoma-upregulated protein - SEQ ID 1886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Example; SEQ ID NO 8; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ19067 standard; protein; 328
              18-OCT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-042477P.
08-NOV-2002; 2002US-0424881P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                Jagged-1 or GPR-32).
                                                                                                         (TOLE-) TOLERRY INC.
                                                                                                                                                       Szymanska G;
                                                                                                                                                                                                    2004-340801/31.
                                                                                                                                                                                                                                               GENBANK; 6650105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 328 AA;
                                                                                                                                                                                                  WPI; 2004-340801
N-PSDB; ADO05707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ19067;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                         Rao P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
ADQ19067
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                                                                                                                                                                                             The present invention relates to PRO proteins and their coding sequences.
The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, intermediate lymphoma, follicular lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO protein as responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylltis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KDSEIFTWAGILGESVTFPWNIQEPROVKIIAWTSKTSVAYVTEGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T cell; antiallergic; immunosuppressive; virucide; antibacterial; antiparasitic; cytostatic; gene therapy; human; CD83; leukocyte differentiation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1019; DB 8; Best Local Similarity 100.0%; Pred. No. 6.7e-88; Matches 199; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte differentiation antigen CD84.
                                                                                                                                                              Claim 10; Fig 109; 695pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO05708 standard; protein; 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-2002; 2002US-0417102P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-2003; 2003WO-US032065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
       WPI; 2004-329389/30
                          N-PSDB; ADL82906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2004
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AD005708;

RESULT 4

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Wood WI;

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual data and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarched of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic sarcoma, possibly via gene therapy or vaccine production. The nucleic fact sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 MASVNSTCNVTLTCSVEKEERAVTYNWSPLGEEGAVLQIFQIFQTPEDQELTYTCTAQNPVSN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                                                                                                                                                                                                                                                          :ly detection of soft tissue sarcoma comprises determining expression a gene in a first soft tissue sample and a normal soft tissue sample I comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1039; DB 8; Length 328; larity 100.0%; Pred. No. 6.7e-88; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 1886; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP23943 standard; protein; 328 AA.
                                                                                                                                                                                                         Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO polypeptide SEQ ID NO:1121.
                                                                                26-NOV-2003; 2003WO-US038193.
                                                                                                                         26-NOV-2002; 2002US-0429739P.
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                                                                                                                                                                                                         Ginsburg WM,
                                                                                                                                                                                                                                                WPI; 2004-441208/41.
                                                                                                                                                                                                                                                                                          Early detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 199; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 328 AA;
WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                         10-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                         Aziz N,
g
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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antidiabletic, dermatological, antipsoriatic, antialiergic, antidabletic, dermatological, antipsoriatic, antialiergic, antidabletic, dermatological, antipsoriatic, antidabletic, dermatological, antipsoriatic, antidabletic, dermatological, be polypeptide, its of the invention may have a use in gene therapy. The PRO polypeptide, its of the invention may have a use in gene therapy. The PRO polypeptide, its of the invention may have a use in gene therapy. The PRO polypeptide, its of the invention may have a use in gene therapy. The PRO polypeptide, its of antidable is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, osteoarthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, sjogram's syndrome, thromboorytopenial, thyroiditis, diabetes mellitus, immune-mediated area in changed in a changed in a central or peripheral nervous system, idiopathic demyelinating polymeuropathy, Guillain-Barre syndrome, content inflammatory demyelinating polymeuropathy, Guillain-Barre syndrome, inflammatory demyelinating polymeuropathy, Guillainry disease, infectious or autoimmune chronic active hepatitis, primary disease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, contact dermatitis, sclerosing cholangitis, chilaease, arthem multiforme, contact dermatitis, psoriasis, an allergic chisease, asthma, allergic rhintis, attoriaria, an immunologic disease, abullous skin disease, stehma, allergic rhintis, attoriaria, an immunologic disease, bullous, contact dermatitis, food cosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity, urricaria, an immunologic disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein contact disease, graft rejection or contact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a novel isolated nucleic acid and the PRO
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100.0%; Pred. No. 6.7e-88;
iive 0; Mismatches 0;
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                                                                                                                              30-OCT-2003; 2003WO-US034312.
                                                                                                                                                                                 01-NOV-2002; 2002US-0423394P.
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Matches 199; Conservative
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N-PSDB; AAV59674.
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22-AUG-1997;
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12-SEP-1997;
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06-JUN-1997;
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Human, secreted protein; testis; tumour; foetal brain tissue;
fusion protein; cancer; central nervous system; seizure; diagnosis;
neurodegenerative disease.
                                                                               Human secreted protein encoded by gene 164 clone HSAWF26.
                                                                                                                                               Location/Qualifiers
                                 AAW74891 standard; protein; 329 AA.
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Misc-difference 329
/label= unknown
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97US-0040161P.
97US-0040162P.
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                                                                25-JAN-1999 (first entry)
                                                                                                                                  Homo sapiens
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acid molecule designated Gene 164 from the human cDNA clone HSAWF26 (deposited as clone ATCC 97903 and ATCC 209049). The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion proteins by linking to the gene to a human immunoglobulin protein as compared to the human protein only. The invention relates to protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (mucleic acid sequences: AAV59511-V59812; amino acid sequences AAAV314731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polymuclectides. Specific uses are described for each of the 186 polymuclectides, based on which tissues they are most highly expressed in (see AAV59511 for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral isohaemia; anglogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive;
                                                                                                                                                                                                                                                                                            22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAMTSKTSVAYVTPGDSETAPVVTVTHRNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG95343 standard; protein; 329 AA
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97US-004033P.
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Matches 199; Conservative
                                                                                                                                                                                                  Sequence 329 AA;
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperpoliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, particular disorders e.g. corneal infection. The polypeptides e.g. also be used to aid wound the aling and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotrais. The polypeptides can also be used as a food additive or preservative to carbohydrate, vitamins, minerals, cofactors and other nutritional carbohydrate, vitamins, minerals, cofactors and other nutritional components. The printed specification, but was obtained in electronic format format and directors.
                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;
Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              v isolated human secreted protein for diagnosing, preventing, treating
ameliorating medical conditions and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6420526B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 483; 129pp; English.
97US-0056882P.
97US-0056884P.
97US-0056887P.
97US-005688P.
97US-005688P.
97US-005688P.
97US-0056892P.
97US-005693P.
97US-005693P.
97US-0056910P.
97US-0056910P.
97US-0056911P.
97US-0056911P.
97US-0056911P.
                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
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Matches 199; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preservative.
                                   22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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Human, secreted protein; hyperproliferative disorder; leukaemia;

breast cancer; wound; reproductive disorder; blood-related disorder;

breast cancer; wound; reproductive disorder; blood-related disorder;

wiskott-Aldrich syndrome; autoimmunedeficiency; thymic hypoplasia;

wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

cy miskott-Aldrich syndrome; autoimmuncto's thyroiditis; allergy; asthma;

cy graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;

cy renal disorder; kidney failure; cardiovascular disorder; cytostatic;

cy majna pectoris; cerebral ischaemia; congenital heart defect;

respiratory disorder; neurological disorder; Alzheimer's disease;

parkinson's disease; inflammation; Crohn's disease;

cy municospulant; neuropecterial; haemostatic; thrombolytic;

anticoagulant; neuropectective; thyromimetic; antiallergic;

antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;

cy cerebroprotective; cardiant; nootropic; antiparkinsonian;
             121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN
                                                                                                                                                                                                                                    Region of human secreted protein encoded by cDNA sequence #164.
                                                                                                                                                        ABO34537 standard; protein; 329 AA.
                                                        181 NSDSISARQLCADIAMGFR 199
                                                                              202 NSDSISARQLCADIAMGFR 220
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97US-0040163P.
97US-0040333P.
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97US-0040331P.
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97US-0047582P.
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97US-0047501P
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                                                                                                                                                                                                              22-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory.
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11-APR-1997;
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ABO34537
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23-MAY-1997

YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120

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Gaps

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New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.
                                                                                                                                                                                                           Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Bndress GA, Yu G, Ni J, Feng P, Young PE, Greenen JM, Ferrie AM;
Duan DR, Hu J, Florner KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 483; 260pp; English.
                                                  YU G.
NI J.
FENG P.
YOUNG P. B.
GREENE J. M.
FERRIE A. M.
DUAN D. R.
HU J.
     RUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
                                                                                                                         OLSEN H S.
FISCHER C L.
                                                                                                                                       EBNER R.
BREWER L A.
MOORE P A.
SHI Y.
                                                                                                                                                                                                                                                  WPI; 2003-521800/49.
N-PSDB; ACD82804.
                                                                                                                                                                      LAFLEUR D W
                                                                                                                                                                             (LIYY/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
                            (CART/)
(BEDN/)
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(YUGG/)
(FENG/)
(YOUN/)
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(FERR/)
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The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The invention also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polynucleotide sequences for the secreted proteins. The polypeptide and polynucleotide confidences for the secreted proteins are useful for preventing, treating, andiomosting medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive clisorders, blood-related disorders (e.g. haemophilia or thrombootytopaenia), immunodeficiencies (e.g. yiskot-t-Andrich syndrome or thrombootytopaenia), immunodeficiencies (e.g. graft-versus-host disease, thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease, wiral or bacterial or Hashimoto's thyroiditis), allergies (e.g. asthma), iral or bacterial or fungal infections (e.g. AIDS or sepsis), renal disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina pectoris, carebral ischaemia or congenital heart defects), respiratory continoration or golymodeles (e.g. AIDS or sepsis). The parkinson's disease), and inflammations (e.g. Crohn's disease). The polymucleotide or polympeptide may also be used as vaccine adjuvants. ABO34374-ABO34815 represent human secreted proteins or their fragments. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html Gaps ;0 100.0%; Score 1039; DB 6; Length 329; 100.0%; Pred. No. 6.7e-88; ive 0; Mismatches 0; Indels 0; Sequence 329 AA;

Query Match Best Local Similarity 100. Matches 199; Conservative

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97105 - 0047595P

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97105 - 0047599P

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2000US-0190068P
2001US-00809391
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
YU G.
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17-MAR-2000;
16-MAR-2001;
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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23-MAY-1997;
23-MAY-1997;
06-JUN-1997;
06-JUN-1997;
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22-AUG-1997;
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22-AUG-1997;
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09-OCT-1997;
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22-AUG-1997;
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18-AUG-1997;
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(ROSE/)
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(BEDN/)
(ENDR/)
(YUGG/)
(NIJJ/)
YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
                      82 YERIHALGPNYNLVISDLRMEDAGDYRADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                                      cytostatic; gene therapy; cancer; human; secreted protein
                                                                                                                                                                                                                                  Novel human secreted protein seq id 483.
                                                                                                                                                                      ADI23198 standard; protein; 329 AA
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                                                                                                        202 NSDSISARQLCADIAMGFR 220
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23-MAY-1997;
23-MAY-1997;
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3-MAY-1997;
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23-MAY-1997;
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                                                                                                                                                                                           ADI23198;
            61
                                                                                             181
                                                                                                                                                RESULT 10
ADI23198
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human; secreted protein; cancer; haematopoietic disorder; endocrine disorder; immune system disease; inflammatory disorder.
                                                                                                                                                                                                    970S-0038621P-
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970S-0040162P-
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97US-0048974P.
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            Human secreted protein #164
                                                                                                               US2003225248-A1.
                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                               11-APR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                      11-APR-1997;
11-APR-1997;
                                                                                                                                            04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-1997
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the cDNA sequence; a polynucleotide sequence encoding a polypeptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of polynucleotide that hybridises under stringent conditions to any one of medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer. The is the amino acid sequence of a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 MASVNSTCNVTLTCSVEKEERNVTYNWSPLGEEGNVLQIFQTFEDQELTYTCTAQNPVSN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTÞGDSETAPVVTVTHRNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes an isolated nucleic acid comprising a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAMTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                             Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress CA, Yu G, Ni J, Feng P, Young PE, Greene UM, Ferrie AM;
Duan DR, Hu J, Florence A, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1039; DB 7; Length 329; Best Local Similarity 100.0%; Pred. No. 6.7e-88; Matches 199; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 483; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH74200 standard; protein; 329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSDSISARQLCADIAMGFR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2004 (first entry)
       YOUNG P E. GREENE J M. FERRIE A M. DUAN D R. HU J. FLORENCE K A.
                                                                                                                                                                                                                                                                                         Duan DR, Hu J, Flore
Brewer LA, Moore PA,
                                                                                              OLSEN H S.
FISCHER C L.
BREWER R.
MOORE P A.
SHI Y.
LAFLEUR D W.
                                                                                                                                                                                                                                                                                                                                        WPI; 2003-898535/82.
                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADI22889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 329 AA;
                                                                                                                                                                                                                  ZENG Z.
KYAW H.
                                                                                                                                                                                                                                                                                                                                                                                                                  e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH74200;
                                                                                                                                                                                                    (LIYY/)
(ZENG/)
(KYAW/)
                                                    (DUAN/)
(HUJJ/)
(FLOR/)
                                                                                                               (FISC/)
(EBNE/)
         (YOUN/)
(GREE/)
(FERR/)
                                                                                                   OLSE/)
                                                                                                                                            BREW/)
                                                                                                                                                            MOOR/)
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셤 ठे 셤 ò g ò

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The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPs) they encode. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoietic disorders, endocrine disorders, diseases of the immune system, inflammatory disorders and many others. Full details of disorders that may be prevented, diagnosed and/or treated by the above methods are given in the specification. The nucleic acid molecules may be used to produce their proteins. The nucleic acid and it's complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The SPs may also be used as antigens in the production of antibodies against the proteins and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Soppet DR, Carter KC, Bedn.
, Yu G, Ni J, Feng P. Young PE, Grev
u J. Florence KA, Olsen HS, Fischer CI
Moore PA, Shi Y, Lafleur DW, Li Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 483; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aberrant expression and activity.
                                                                                                                                                                                               97135 - 0056876P
97135 - 00568778P
97135 - 00568878P
97135 - 0056881P
97135 - 0056881P
97135 - 0056882P
97135 - 0056882P
97135 - 0056888P
97135 - 0056888P
97135 - 0056888P
97135 - 0056888P
97135 - 0056888P
97135 - 0056898P
97135 - 0056898P
97135 - 0056898P
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97135 - 0056898P
97135 - 0056898P
97135 - 0056898P
97135 - 0056898P
97135 - 0056898P
97135 - 0056898P
97US-0051926P.
97US-0052874P.
97US-0056630P.
97US-0056631P.
97US-0056631P.
97US-0056631P.
97US-005664P.
97US-005664P.
97US-005684P.
97US-005684P.
97US-005684P.
97US-005684P.
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7US-0058785P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00149476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7US-0061060P
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Duan R, Hu J,
                                                                                                                                                             22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997,
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22-AUG-1997
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                                   22-AUG-19
22-AUG-19
22-AUG-19
22-AUG-19
22-AUG-19
22-AUG-19
22-AUG-19
                                                                                                                                                                                                                                                                  22-AUG-1
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22-AUG-1
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22-AUG-1
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/label= RLRKPKITWSLRHSEDGICRISLTCSVEDGGNTVMYTWTPLQKEAVVSQ
GESHLMVSWRSSENHPNLTCTASNPVSRSSHQFLSENICSG
/note= "Optionally absent"
                                                                                                                                                                                                                                                                                YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
                                                                                                                                                                                                                                                                                                  MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                                                                                                                                                                                                                                                                                                                                 assays to identify modulators of SP expression and activity. The anti-SP antibodies and antagonists may also be used to down regulate expression and activity. The anti-SP antibodies may also be used as diagnostic agents for detecting the presence the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The present sequence represents the amino acid sequence of a human secreted protein.
                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; anorectic; virucide; antibacterial; fungicide; protozoacide; mootropic; neuroprotective; antiparkinsonian; protozoacide; nootropic; neuroprotective; antiparkinsonian; dermatological; antiasthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGFR4; complement factor I precursor; matrix metalloproteinase-15 precursor; MDC3; T-lymphocyte surface antigen Ly-9 precursor; fibroblast growth factor-21; FGF-21; alpha-2 macroglobulin-like polypeptide variant; antileukoproteinase 1 precursor; LiV-1; nuclear hormone receptor NOR-1; transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
                                                                                                                                                                                                                                  22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                               KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                 Gaps
                                                                                                                                                                                 ö
                                                                                                                                                 Length 329;
                                                                                                                                                                                 Indels
                                                                                                                                                 100.0%; Score 1039; DB 8;
100.0%; Pred. No. 6.7e-88;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL57243 standard; protein; 526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOV5c protein SEQ ID NO:188.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NSDSISARQLCADIAMGFR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Ser, Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Glu, Lys
                                                                                                                                                                                                                                                                                                                                                                                                                NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004 (first entry)
                                                                                                                                                                                    Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 489
                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004022723-A2
                                                                                                                      Sequence 329 AA;
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                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrie AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bednarik DP;
, Greene JM, Fe
cher CL, Ebner R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zeng Z,
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09-SEP-2003; 2003WO-US028141

18-MAR-2004.

63 YLGRLDITKWSYSLCISNLTINDAGSYKAQINQRNPEVTTEBEFTLFVYEQLQEPQVTMK 122 SLMASVNSTCNVTLICSVEKEEKNVTYNWSPL-----GEEGNVLQIFQTPEDQELTYTC 172

TAONPVSNNSD-SISARQLCAD 193 183 TAONPVSORSSLPVHVGOFCTD 204

173

8

g

119

a ò 셤

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ADL57105 standard; protein; 526

RESULT 13 ADL57105

60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKIT-Q 118

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The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequence [W1] y defined in the specification. A polypeptide of the invention has antidiabetic, anoretic, cardiant, hypotensive, antiaterenial, individe, indibaterial, fungicide, protozoacide, notropation, antipaterial, fungicide, protozoacide, notropation, antipaterial, fungicide, protozoacide, notropatici, antipaterial, and protocopical, antiasthmatic, and antipaterial of a medicament for triasthmatic, and antibodies are useful in the manufacture of a medicament for relating a syndrome associated with a human disease, preferably a NOVA-associated Misorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, clabeles, pestry, infectious diseases up at manufacture of a medicament for treating, preventing or diagnosing diseases up antipated associated with a human disease, preferably a NOVA-associated disorders, inflammator, and protozoally anorexia, and articopies are netabolic disorders, clabeles, pestry, infectious diseases (inflammatory skin disorders, consecutation, and protozoally anorexia, inflammatory skin disorders, inflammatory skin disorders, inflammatory skin disorders, inflammatory skin disorders, inflammatory skin disorders, inflammatory skin disorders, inflammatory skin disorders, and protozoally anorexias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules or the modulate or inhibit e.g. neurogenesis, cell differentiation, haematopolesis, wound healing and angiogenesis, in generators for use in therapeutic or disapnoses (methods: The NOVA publicates of the invention of antibodies that the bid angiogenesis, in chromosome mapping, preventive medicine show homology to efficient and protosy to mally preventive medicine and protosy to mally preventive medicine and protosy to mally prevented as hybridisation protosy. In the precursor; NOV8a-5s show
                                                                                                                                                                                                                                                                                                                                                 New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                                                                                                                                                                                                                                  Rieger DK;
                                                                                                                                                                                                                                                                  Padigaru M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; SEQ ID NO 188; 214pp; English.
                                                                                                                                                                                                                                                                  Ort I,
                                                                                                                                                                                                                                                                  Guo X, Anderson DW,
                                                                                      23 - SEP-2002; 2002US-0412766P.
23 - SEP-2002; 2002US-0412825P.
24 - SEP-2002; 2002US-0412767P.
25 - SEP-2002; 2002US-0413342P.
                        10-SEP-2002; 2002US-0409544P.
12-SEP-2002; 2002US-0410320P.
16-SEP-2002; 2002US-0411060P.
                                                                                                                                                                              30-SEP-2002; 2002US-0414832P.
2002US-0409145P.
                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                           WPI; 2004-315567/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 526 AA;
                                                                                                                                                                                                                                                                  Zhong M,
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human; antidiabetic; anorectic; cardiant; hypotensive;

Human NOV5b protein SEQ ID NO:50.

03-JUN-2004 (first entry)

ADL57105;

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The invention relates to a novel isolated polypeptide (NOVX) comprising mature form of any of the 37 amino acid sequences fully defined in the specification. A polypeptide of the invention has antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, virucide, antibacterial, fungicide, protozoacide, nootropic,
                                                                                                              numnan; autolateric; autorectic; catulatic; importerial; fungicide; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; antiooroutlaent; osteopathic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGR4; complement factor Iprecursor; metaloproteinase-15 precursor; MDC3; T-lymphocyte surface antigen Ly-9 precursor; fibroblast growth factor-21; FGF-21; fibroblast growth factor-21; FGF-21; antileukoproteinase 1 precursor; LiV-1; nuclear hormone receptor NOR-1; transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhong M, Guo X, Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002US-0410320P.
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2002US-0412825P.
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2002US-0413342P.
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N-PSDB; ADL57104.
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12-SEP-2002;
16-SEP-2002;
23-SEP-2002;
23-SEP-2002;
24-SEP-2002;
25-SEP-2002;
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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1 KDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTS-KTSVAYVTPGDSETAPVVTVTHRN 59

33.9%; Score 352; DB 8; Length 526; 38.1%; Pred. No. 8.4e-24;

62

14; Gaps

Indels

70;

41; Mismatches

Query Match
Best Local Similarity 38.19
Matches 77; Conservative

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redroptorectry, antinflammatory, dermatological, antiasthmatic, antinflammatory, dermatological, antiasthmatic, antinflammatory, dermatological, antiasthmatic, antinflammatory, dermatological, antiasthmatic, antilipaemic activity. A polymocleotide of the invention may have a use in gene therapy. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome cassociated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, conference). And protozoall, anorexia, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, epilepsy; immune disorders, Alzheimer's disease, Parkinson's disease, epilepsy; immune disorders, Alzheimer's contexthritis), haematopoietic disorders, inflammatory skin disorders, asthma, and various dyslipidaemias. The nucleic acids and polypeptides cathat modulate or inhibit e.g. neurogenesis, call differentiation, cell contiferation, haematopoiesis, wound healing and angiogenesis, in generation of antibodies that bind immunospecifically to NoVX usbasnances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The NoVX cortain known human proceins NoV1a-1t show homology to citizonely growth factor receptor 4 (FGFR4); NOV2a shows homology to methology to fibroblast growth factor-21 collyaptions in NoVa-1 show homology to fibroblast growth factor-21 collyaptions. In NoVa-2 show homology to although the although to a precursor; NOV4a show show homology to although the although the above antigen by an acide antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor; NOV9a-91 show homology to LIV-1 protein; NOV10a shows homology to nuclear hormone receptor NOR-1; NOV11a-11] show homology to transmembrane protein-like; NOV12a-12c show homology to beta-necendorphin precursor. The present sequence represents a NOVX polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention.
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60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKIT-Q 118 63 YLGRLDITKWSYSLCISNLTLANDAGSYKAQINQRNFEVTTEEBFTLFVYEQLQEDQVTMK 122 SLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEEGNVLQIFQTPEDQELTYTC 172 1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVAYVTPGDSETAPVVTVTHRN 59 ; Score 352; DB 8; Length 526; ; Pred. No. 8.4e-24; 41; Mismatches 70; Indels 173 TAQNPVSNNSD-SISARQLCAD 193 183 TAONPVSORSSLPVHVGOFCTD 204 33.9%; Query Match
Best Local Similarity 38.1
Matches 77; Conservative 119 셤 ઠ 셤 ઠે 염 8 셤 ଚ

Sequence 526 AA;

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Immunoglobulin superfamily protein; IGSFP; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis; primary thrombocytopenia; cancer; leukaemia; lymphoma; sarcoma; myeloma; autoimmune disorder; inflammatory disorder;
                                                                                                                          Human immunoglobulin superfamily protein IGSFP-8.
               ABG96270 standard; protein; 551 AA.
                                                                                      (first entry)
                                                                                        11-DEC-2002
ABG96270
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The present invention relates to new immunoglobulin superfamily proteins

(IGSFP). The polypeptides, polynucleotides, agonists and antagonists are

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(I 60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKIT-Q 118 New human immunoglobulin superfamily proteins and polynucleotides, useful for diagnosing, treating or preventing disorders with aberrant IGSFP expression, such as autoimmune, inflammatory or cell proliferative 1 KDSEIFTVNGILGESVTPPVNIQEPROVKIIAWTS-KTSVAYVTPGDSETAPVVTVTHRN 59 autoimmune thyroiditis; contact dermatitis; Crohn's disease; diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout; Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis; tester's syndrome; rheumatoid arthritis; Sjogren's syndrome; uveitis; trauma; viral infection; bacterial infection; fungal infection; parasitic infection; protozoal infection; helminthic infection; Yang J; 14; Gaps Thangavelu K, Warren BA, Tang YT, Duggan BM; nn MR, Honchell CD, Burford N, Forsythe IJ, DB 5; Length 551; 33.9%; Score 352; DB 5; Length 551 38.1%; Pred. No. 9e-24; ive 41; Mismatches 70; Indels Claim 1; Page 129-130; 145pp; English. 12-MAR-2001; 2001US-0275249P. 31-AUG-2001; 2001US-0316B10P. 21-SEP-2001; 2001US-032977P. 26-OCT-2001; 2001US-0343880P. 12-MAR-2002; 2002WO-US009052 (INCY-) INCYTE GENOMICS INC. Query Match
Best Local Similarity 38...
Best 77; Conservative Baughn MR, WPI; 2002-723340/78. gene therapy; human N-PSDB; ABS76363. Sequence 551 AA; Xu Y, WO200272794-A2. Ното варіепв. 19-SEP-2002 48 diseases. Tran UK, Yue H, Mason ð 유 ò

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SIMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEEGNVLQIFQTPEDQELTYTC 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated immune response associated proteins (IRAP) polypeptide and polymuclectide, useful for diagnosing and/or treating disorders with aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer and stroke.
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                                                                                                                                                                                                                                                                                                                             immune response associated protein; IRAP; antiarteriosclerotic; cytostatic; neuroprotective; antiparkinsonian; hepatotropic; ecebroprotective; antiinflammatory; nootropic; vasotropic; arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease; Parkinson's; Grohn's; gene therapy; human.
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Pred. No. 9.3e-24;
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Maximum DB seq
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Perfect score:
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Sequence 6428, Application US/09949016
; Sequence 6428, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VEWTER, J. Czaig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PLILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 6428
LENTH: 328
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2, Appl
2, Appli
20, App
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Sequence 36, Appl
Sequence 6484, Ap
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100.0%; Pred. No. 1.2e-101;
ive 0; Mismatches 0;
US-09-199-955-10

US-08-880-875-10

US-09-513-999C-4353

US-09-36-2-48A-2

US-09-905-125A-320

US-09-905-775A-320

US-09-906-775A-320

US-09-906-775A-320

US-09-906-775A-320

US-09-906-775A-320

US-09-906-775A-320

US-09-906-775A-320

US-09-906-181A-320

US-09-906-181A-320

US-09-906-181A-320

US-09-949-016-6907

US-09-949-016-6907

US-09-949-016-6307

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Best Local Similarity 100.
Matches 199; Conservative
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APPLICANT: Rosen et al. TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P1 PILING DATE: 1998-09-08
APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1000-0 CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT PILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/0449
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,634
EARLIER APPLICATION NUMBER: 60/040,636
EARLIER APPLICATION NUMBER: 60/040,636
EARLIER APPLICATION NUMBER: 60/040,636 R APPLICATION NUMBER: 60/047, 600

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 615

R APPLICATION NUMBER: 60/047, 615

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 597

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 502

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047, 503

R FILING DATE: 1997-05-23

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R FILING DATE: 1997-05-23
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R RELING DATE: 1997-05-23
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ER APPLICATION NUMBER: 60/040,333
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ER APPLICATION NUMBER: 60/040,621
ER FILING DATE: 1997-03-07
ER APPLICATION NUMBER: 60/040,626
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ER FILING DATE: 1997-03-07
ER APPLICATION NUMBER: 60/040,336
ER FILING DATE: 1997-03-07
ER APPLICATION NUMBER: 60/040,163
ER FILING DATE: 1997-03-07
ER APPLICATION NUMBER: 60/040,163
ER FILING DATE: 1997-03-07 FILING DATE: 1997-04-11 APPLICATION UNDBER: 60/043,314 LING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,568 GENERAL INFORMATION: EARLIER SARLIER SARLIER SARLIER

R APPLICATION NUMBER: 60/056,874
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,910
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,864
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/043,315
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/048,974
R APPLICATION NUMBER: 60/056,886
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,877
R APPLICATION NUMBER: 60/056,877
R APPLICATION NUMBER: 60/056,877
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R APPLICATION NUMBER: 60/056,889
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,630
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R PPLICATION NUMBER: 60/056,662
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22 APPLICATION DATE: 1997-05-23
APPLICATION NUMBER: 60/047,599
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,588
FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22
APPLICATION UNDBER: 60/056,903
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION UNDHER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,894 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,313
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,761 APPLICATION NUMBER: 60/047,595 APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 1997-08-22 1997-08-22 1997-04-11 FILING DATE: 1997-04-11 FILING DATE: 1997-08-2 APPLICATION NUMBER: FILING DATE: EARLIER
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FARENAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-04

SPRIOR FILING DATE: 2000-10-08

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7327
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Pred. No. 1.2e-101;
; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER PILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,929
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EARLIER APPLICATION NUMBER: 60/051,929
EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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US-09-949-016-7327; Sequence 7327, Application US/09949016; Patent No. 6812339
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Patent No. 6342581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R APPLICATION NUMBER: 60/047,586
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,590
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,594
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,594
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,593
R APPLICATION NUMBER: 60/047,614
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,614
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
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R APPLICATION NUMBER: 60/056,632

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,876

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,876

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,881

R APPLICATION NUMBER: 60/056,999

R APPLICATION NUMBER: 60/056,999

R FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/043,670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 OSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFOTPEDQELT 169
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                                                                                                               67
                                                                                                                                                     30 VVAVLQESISLPLEIPPDEEVENIIWSHKSLATVVPGKEGHPATIMVTNPHYQGQVSFL 89
                                                                                                             8 VNGILGESVTFPVNIQEPROVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHAL
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                                                                     Gaps
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Gan B.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
THREE OF INVENTION: ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                               90 DPXYSLHISNLSWEDSGLYQAQVNLRTSQISTWQQYNLCVYRWLSE 135
                                                                                                                                                                                                        68 GPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGK 113
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15.4%; Score 160; DB 1; Length 298;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels
                         Length 143
                                                                 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CALLICLE
COUNTRY: USA
ZUP: 94304-1104
ZUP: 94304-1104
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-US44
FILING DATE: 02-DEC-US44
                    17.5%; Score 182; DB 3;
35.8%; Pred. No. 2.1e-11;
live 24; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08348792; Patent No. 5576423; GENERAL INFORMATION:
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Query Match
Best Local Similarity 35.00,
Thes 38; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34.0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 298 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 298 amino acid
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STATE: California
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US-08-348-792-4
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OTHER INFORMATION: Xaa equals stop translation
.09-227-357-192
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EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
                    R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,916

R FILING DATE: 1997-07-08

R PILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,918

R APPLICATION NUMBER: 60/051,918

R APPLICATION NUMBER: 60/051,920

R APPLICATION NUMBER: 60/051,920

R APPLICATION NUMBER: 60/051,920
                                                                                                                                                                                                                      REPLICATION NUMBER: 60/052,733
REPLING DATE: 1997-07-08
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APPLICATION NUMBER: 60/055,684
FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
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ORGANISM: Homo sapiens
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LOCATION: (138)
OTHER INFORMATIC
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NAME/KEY: SITE
LOCATION: (143)
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NAME/KEY: SITE
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LENGTH: 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 LGSKVLLPLTYERINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 IGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVHRN 59
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                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08462738
; Sequence 4, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
    APPLICANT: Aversa, Gragorio
    APPLICANT: Cocks, Benjamin G.
    APPLICANT: Cocks, Benjamin G.
    APPLICANT: Go Vries, Jan SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
    TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
    NUMBER OF SEQUENCES: 12
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: DNAX Research Institute
    STREET: 901 California Avenue
    CITY: Palo Alto
    CONTANTIONED CONT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIPICATION THESE: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIPICATION: 435
PRIOR APPLICATION THESE: US/08/348,792
FILING DATE: 02-DEC-1994
ATTOWNEY/AGENT INFORMATION:
NAME: Ching, Edwin P: REGISTRENCE/DOCKET NUMBER: 34,090
REGISTRENCE/DOCKET NUMBER: 34,090
REJERBRENCE/DOCKET NUMBER: 34,090
TELERBRANICATION INFORMATION:
TELERBRANICATION INFORMATION:
TELERBRANICATION THORMATION:
TELERBRANICATION THORMATION:
TELERBRANICATION TO TO TO TO TO THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 YICTVSNPISNNSQTFS 223
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                                                               207 YICTVSNPISNNSQTFS 223
170 YTCTAONPVSNNSDSIS 186
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amino acid
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Best Local Similarity 25.4%
Matches 50; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-462-738-4
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                                              GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Jan E.
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARA Research Institute
STREET: 901 California Avenue
CUITY: Palo Alto
COUNTRY: USA
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15.4%; Score 160; DB 3; Length 298;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1104

ZIP: PABDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: PREM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
APPLICATION NUMBER: US 08/461,473
FILING DATE: 02-DEC-1994
ATORNEY/AGENT INCEMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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Sequence 4, Application US/09199955
Patent No. 6372899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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PURIFIED GENES ENCODING MAMMALIAN CELL SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
                                                                                                                                                       STATE: CALLILLIANCE
COUNTRY: USA
ZIP: 93404-1104
ZIP: 93404-1104
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compacible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:: US/08/348,792
FILING DATE: 02-DEC-1994
CLASSIFICATION: SOF DEC-1994
CLASSIFICATION: Bewin P.
REPRENCES DOCKET INFORMATION:
REPRENCES DOCKET NUMBER: DX0436
TELECOMMUNICATION INFORMATION:
TELEFRAX: 415-496-1200
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
FRANGTH: 305 amino acids
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  TITLE OF INVENTION: PURIFIED GENES EN TITLE OF INVENTION: SURFACE ANTIGENS; NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 YTCTAQNPVSNNSDSIS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 305 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-348-792-6
                                                                                                                             CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POPOLOGY:
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APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: LAST CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 298;
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                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78;
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CLASSIFICATION: 435
PRICKATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-48-1200
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08348792
Patent No. 2576433
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocke,
APPLICANT: Cocke, Benjamin G.
APPLICANT: de Vries, Jan E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-880-875-4
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99 YLE------NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08462738;
Sequence 6, Application US/08462738;
Patent No. 5977303;
GENERAL INFORMATION:
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Govers, Benjamin G.
APPLICANT: Govers, PRIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: PRIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES;
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARK Research Institute
CORRESPONDENCE ADDRESS:
Query Match 15.4%; Score 160; DB 1; Length 305; Best Local Similarity 25.4%; Pred. No. 1.4e-08; Matches 50; Conservative 35; Mismatches 78; Indels
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60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
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| Sequence 6. Application US/0880875
| Patent No. 6339065
| GENERAL INFORMATION:
| APPLICANT: Aversa, Gregorio APPLICANT: Cocks, Benjamin G. APPLICANT: Cocks, Benjamin G. APPLICANT: Cocks, Benjamin G. APPLICANT: TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES NUMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRE
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
FILING DATE:
CLASSIFICATION: 435
                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDAER:
APPLICATION UNDAER:
FILING DATE: 05-UIN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAMME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
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901 California Avenue
                           APPLICATION NUMBER: US/09/199,955
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET UNMER: DX04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 305 anino acids
TUDENCE: TELEPHONE CHARACTERISTICS:
TENGTH: 305 anino acids
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STATE: California
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STREET: 90
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US-08-880-875-6
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SUBFACE ANTIGENS: PROTEINS AND ANTIBODIES
TORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
15.4%; Score 160; DB 2; Length 305;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: FI-loppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PSTSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: O5-JUN-1995
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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901 Californía Avenue
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APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-199-955-6; Sequence 6, Application US/09199955; Patent No. 6372899; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 YTCTAQNPVSNNSDSIS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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STATE: California
COUNTRY: USA
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71 YLE-----NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 119
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Patent No. 5977303
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: PUNIETED GENES ENCODING MAWMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                          Length 307;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    ; Score 160; DB 1;
; Pred. No. 1.4e-08;
35; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 YTCTAQNPVSNNSDSIS 186
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179 YICTVSNPISNNSQTFS 195
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             TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.4%;
                                        TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INPORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 307 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 307 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Conservative
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                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-348-792-8
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Resect
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-462-738-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 OSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFOTPEDOELT 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 LGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08348792
; Sequence 8, Application US/08348792
; Patent No. 557643
; GENERAL INFORMATION:
   APPLICANT: Aversa, Gregorio
   APPLICANT: Chang, Chia-Chun J.
   APPLICANT: Cocks, Benjamin G.
   APPLICANT: Cocks, Benjamin G.
   APPLICANT: Cocks, Benjamin G.
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   APPLICANT: Cocks, Benjamin G.
   APPLICANT: Cocks, Benjamin G.
   APPLICANT: Cocks, Benjamin G.
   APPLICANT: Cocks, Benjamin G.
   APPLICANT: Cocks, Benjamin G.
   APPLICANT: Cocks, Benjamin G.
   STREST: 901 California Avenue
   STRET: Palo Alco
   STRET: Palo Alco
   STRET: California
   COMPTY: Palo Alco
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 34,090
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHMONE: 415-496-1200
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION WUMBER: 34,09
REFERENCE/DOCKET NUMBER: D
                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 305 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      6 TYPE: amino acide TOPOLOGY: 11-
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                                                                                                                                                                                                                                                                                                                                            71 YLE-----NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 119
                                                                                                                                                                                                                                                                                                                                                                                                             118 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 169
                                                                                                                                                                                                                                                                                                              60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
                                                                                                                                                                                                                  12 LGESVTPP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN 59
                                                                                                                                                                                                                                                  11 LGSKVLLPLTYBRINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 70
                                                                                                                                                                     78; Indels 34; Gaps
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Sequence 8, Application US/09199955

Patent No. 6372899

GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: FURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP.
                                                                                                                Query Match
15.4%; Score 160; DB 2; Length 307;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/461,473
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAMB: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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179 YICTVSNPISNNSQTFS 195
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-738-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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RESULT 1
US-10-104-943-4
                                                                   February 4, 2005, 12:15:12; Search time 65.5796 Seconds (without alignments) 988.338 Million cell updates/sec
                                                                                                                     US-09-882-171-483_COPY_22_220
1039
1 KDSEIFTYNGILGESVTFPV.......NNSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                        1373511
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                         1373511 segs, 325702437 residues
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Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 4, Appli Sequence 30, Appl Sequence 483, App Sequence 483, App Sequence 8, Appli Sequence 11, Appli Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 82, Appli Sequence 82, Appli Sequence 82, Appli Sequence 82, Appli Sequence 82, Appli Sequence 82, Appli Description US-10-104-943-4
US-10-446-523-30
US-09-809-391-483
US-09-809-171-483
US-10-164-861-483
US-10-104-861-483
US-10-104-943-7
US-10-328-538-2
US-10-436-523-77
US-10-436-523-77 Query Match Length DB 100.0 100.0 100.0 100.0 33.9 1039 1039 1039 1039 353 343.5 343.5 343.5 343.5 Result

18 91 91 91 91 91 91 91 91 91 91 91 91 91	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	76,	Sequence 76, Appl Sequence 76, Appl
US-10-220-946 US-10-436-523 US-10-436-523 US-10-436-523 US-10-170-385 US-10-436-523	10-436-523-19 10-436-523-19 10-436-523-19 10-436-523-19 10-436-523-3 10-64-237-2 10-64-853-3	US-10-245-752- US-10-245-859- US-10-245-107- US-10-245-107- US-10-245-143- US-10-245-771- US-10-245-771-	US-10-245-883-7 US-10-237-835-7 US-10-238-283-7 US-10-238-370-7 US-10-245-147-7 US-10-245-147-7 US-10-245-130-7 US-10-245-130-7 US-10-245-130-7 US-10-245-130-7 US-10-245-130-7
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11 11 11 11 10 10	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	22 23 23 24 24 24	

ALIGNMENTS

; Sequence 4, Applicat; Publication No. US20	Sequence 4, Application US/10104943 Publication No. US20030092017A1 EXEMPDAL THROMATION	
APPLICANT: B:	APPLICANT: Bristol APPLICANT: Bristol THE TANDERS OF TANDERS OF THE POST OF THE PROPERTY MAINOGLOBILIN SUPERFAMILY MEMBE	MBE
; TITLE OF INVENTION:	INTION: and VARIANTS AND SPLICE VARIANTS THEREOF	
, FILE REFERENCE: D0135 NP	E: D0135 NP	
, CURRENT APPL	CURRENT APPLICATION NUMBER: US/10/104,943	
CURRENT FILLI	COKREWY FILLING DATE: 200-203-22 DETOD ADDITCATION NIMBER: IIS 60/278 037	
PRIOR FILING	FILING DATE: 2001-03-22	•
; PRIOR APPLIC	PRIOR APPLICATION NUMBER: US 60/281,223	
; PRIOR FILING	PRIOR FILING DATE: 2001-04-03	
; NUMBER OF SE	NUMBER OF SEQ ID NOS: 129	
; SOFTWARE: Pa	SOFTWARE: Patentin version 3.0	
; SEQ ID NO 4		
; LENGTH: 328		
; TYPE: PKT ; ORGANISM: Homo sapiens	omo sapiens	
US-10-104-943-4		
Query Match	100.0%; Score 1039; DB 14; Length 328;	
Best Local Similarity Matches 199; Conser	rative 0;	
0y 1 K	1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY 60	
Db 22 K	KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY 81	
δλ (91 <u>γ</u>	YERIHALGENYNLVISDLEMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120	
T 82 X	YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141	
Qy 121 M	121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180	

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Query Match
Best Local Similarity 100.0
Matches 199; Conservative
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US-09-882-171-483
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61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
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TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
FILE REFRENCE: 7833-244-999
CURRENT APPLICATION NUMBER: US/10/436,523
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: US/10/007,303
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1039; DB 14; Length 328; llarity 100.0%; Pred. No. 3.8e-89; Conservative 0; Mismatches 0; Indels 0;
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Sequence 483, Application US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
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FRATURE:
INAME/KEY: SITE
I. LOCATION: (329)
CHER INFORMATION: Xaa equals stop translation
US-09-809-391-483
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Publication No. US20030180888A1
GENERAL INFORMATION:
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Matches 199; Conserv
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121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
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                                                                                        Gaps
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    DB 10; Length 329;
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FILE REPRENCE: PSOUGE2
FULKE REPRENCE: PSOUGE2
FULKE REPRENCE: PSOUGE2
FULKE APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
FRIOR APPLICATION NUMBER: 09/809,391
FRIOR APPLICATION NUMBER: 09/149,476
FRIOR PELLING DATE: 1998-0-06
FRIOR FILING DATE: 1998-0-06
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FRIOR FILING D
100.0%; Score 1039; DB 10
100.0%; Pred. No. 3.8e-89;
iive 0; Mismatches 0;
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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FILING DATE: 1997-05-23
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PRIOR APPLICATION NUMBER: 60/047,584
PRIOR APPLICATION NUMBER: 60/047,500
PRIOR APPLICATION NUMBER: 60/047,500
PRIOR PAPLICATION NUMBER: 60/047,520
PRIOR PAPLICATION NUMBER: 60/047,529
PRIOR PAPLICATION NUMBER: 60/047,529
PRIOR PELING DATE: 1997-05-23
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R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,589

R APPLICATION NUMBER: 60/047,589

R APPLICATION NUMBER: 60/047,593

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R APPLICATION NUMBER: 60/047,614

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/043,578

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,576

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R APPLICATION NUMBER: 60/043,576 R APPLICATION NUMBER: 60/056,636
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,874
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,910
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,864
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631
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R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/047,599
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,588
R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/043,670

R FILING DATE: 1997-04-11

R FILING DATE: 1997-08-22

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R FILING DATE: 1997-08-22
R PPLICATION NUMBER: 60/056,880
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R APPLICATION NUMBER: 60/056,894
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R APPLICATION NUMBER: 60/056,81
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,590
APPLICATION NUMBER: 60/047,590
FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,862 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 APPLICATION NUMBER: 60/056,909 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-08-22 PRIOR

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Sequence 483, Application US/10164861

PUDLication No. US20030225248A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: PZ002P1

CURRENT FILING DATE: 2002-06-10

FRIOR APPLICATION NUMBER: US/10/149,476

FRIOR APPLICATION NUMBER: PCT/US98/04493

FRIOR FILING DATE: 1998-09-08

FRIOR FILING DATE: 1998-03-06

NUMBER FOL SEQ ID NOS: 757

SOFTWARE: PATENTIN OF NOS: 757
                                                                                                                Query Match
100.0%; Score 1039; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 199; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 199; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: Xaa equals stop translation
US-10-164-861-483
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05
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FEATURE:
NAME/KEY: SITE
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LENGTH: 329
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60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKIT-Q 118
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Publication No. US20030054002A1
GENERAL INFORMATION:
APPLICANT: WAKELAND, WARD
APPLICANT: WANDSTRAIT, AMY
APPLICANT: WOREL, LAURENCE
TITLE OF INVENTION: IN IMMUNE TOLERANCE
TITLE OF INVENTION: IN IMMUNE TOLERANCE
FILE REFERENCE: UTSD:722US
CURRENT APPLICATION NUMBER: US/09/860,836B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVAYVTPGDSETAPVVTVTHRN
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                                                                                                                     APPLICANT: YUE, Henry; XU, Yuming;
APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
APPLICANT: TANG, Y. Tom; DUGGAN, Barendan M.;
APPLICANT: TANG, Y. Tom; DUGGAN, Barendan M.;
APPLICANT: TRAN, Uyen K.; BAUGHN, Mariah R.;
APPLICANT: TRAN, Uyen K.; BAUGHN, Mariah R.;
APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
ITILB OF INVENTION: IMMUNGIGNBLIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-0925 USN
CURRENT APPLICATION NUMBER: US/10/471,449
CURRENT APPLICATION NUMBER: US/20/9052
PRIOR APPLICATION NUMBER: US 60/275,249
PRIOR APPLICATION NUMBER: US 60/316,810
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-03-1
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-11-02
NUMBER OF SEQ. ID NOS: 24
SUFTWARE: PERL PROGRAM
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33.9%; Score 352; DB 15;
Best Local Similarity 38.1%; Pred. No. 2.6e-24;
Matches 77; Conservative 41; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7500099CD1
US-10-471-449-8
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US-10-471-449-8; Sequence 8, Application US/10471449; Publication No. US20040097711A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 2, Application US/10328538

Publication No. US20040109863A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brange, Peter
TITLE OF INVENTION: that express Ly-9
FILE REFERENCE: HYS-68CP
CURRENT APPLICATION UNMBER: US/10/328,538
CURRENT PILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 10/310,612
PRIOR APPLICATION NUMBER: 10/310,612
PRIOR FILING DATE: 2002-12-04
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
                                                                                                               Sequence 2, Application US/10310612;
Publication No. US20040109862A1
GENERAL INFORMATION:
APPLICAT: Emtage, Peter
TITLE OF INVENTION: that express Ly-9
TITLE OF INVENTION: that express Ly-9
TITLE REPERENCE: HYS-62
CURRENT APPLICATION NUMBER: US/10/310,612
CURRENT PILING DATE: 2002-12-04
NUMBER: OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.1%; Score 343.5; DB 16; 36.8%; Pred. No. 2.1e-23; iive 40; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.1%; Score 343.5; DB 1
36.8%; Pred. No. 2.1e-23;
iive 40; Mismatches 74
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         223 AQNPVSQRSSLPVHVGQFCTD 243
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Matches 74; Conservative
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CRGANISM: Homo sapiens
US-10-328-538-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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Sequence 7, Application US/2003092017A1
Sequence 7, Application No. US20030092017A1
Sequence 7, Application No. US20030092017A1
SETILIS OF INVENTION: SQUIDD COMPANY
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL IMMUNOCLOBULIN SUPERFAMILY MEMBER
TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF
FILE REFERENCE: D0135 NP
CURRENT APPLICATION NUMBER: US/10/104,943
CURRENT APPLICATION NUMBER: US 60/278,037
PRIOR APPLICATION NUMBER: US 60/278,037
PRIOR APPLICATION NUMBER: US 60/281,223
PRIOR PILING DATE: 2001-04-03
PRIOR SEQ ID NOS: 129
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 SVKVSENFCNITLMCSVKGAEKSVLYSWTPREPHASESNGGSILTVSRTPCDPDLPYICT 222
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                                                                                                                                                                                                                                                                          Query Match 33.9%; Score 352; DB 10; Length 610; Best Local Similarity 38.1%; Pred. No. 3e-24; Matches 77; Conservative 41; Mismatches 70; Indels 1.
PRIOR APPLICATION NUMBER: 60/204,963
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 11
LENGTH: 610
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Best Local Similarity 36.89
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   8 VNGILGESVIPPVNIQEPROVKIIAWISKTSVAYVIPGDSETAPVVIVTHRNYYERIHAL
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                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 77, Application US/10436523
; Sequence 77, Application US/10436523
; Publication No. US20030180888A1
; GENERALI INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF;
; FILE REFRENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 77
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38.1%; Pred. No. 6.4e-23;
iive 37; Mismatches 69;
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32.0%; Score 332; DB 14;
Best Local Similarity 38.1%; Pred. No. 7.7e-23;
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'Sequence 18, Application US/10220946
'Publication No. US20030124575A1
'GENERAL INFORMATION:
                                                                                                           Query Match
Best Local Similarity 38.1%
         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-523-82
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US-10-436-523-77
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US-10-436-523-79

Sequence 79, Application US/10436523

Fublication No. US20030180888A1

GENERAL INFORMATION:

TITLE OF INVENTION: CD2000 MOLECULES, AND USES THEREOF

FILE REFERENCE: 785-244-98

CURRENT APPLICATION NUMBER: US/10/436,523

CURRENT APPLICATION NUMBER: US/10/436,523

CURRENT APPLICATION NUMBER: US/10/007,303

PRIOR FILING DATE: 2001-11-20

PRIOR FILING DATE: 2001-11-03

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin version 3.1
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| Publication No. US20030180888A1
| GENERAL INFORMATION OF US2003018088A1
| APPLICATION NO. US2003018088A1
| TILLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF FILE REFERENCE: 7853-244-999
| CURRENT APPLICATION NUMBER: US/10/436,523
| PRIOR APPLICATION NUMBER: US/10/007,303
| PRIOR PLILNG DATE: 2001-11-20
| PRIOR PLILNG DATE: 2001-11-20
| PRIOR FILING DATE: 2000-11-20
| PRIOR FILING DATE: 2000-11-03
| NUMBER OF SEQ ID NOS: 100
| NUMBER OF SEQ ID NOS: 100
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32.0%; Score 332; DB 14;
Best Local Similarity 38.1%; Pred. No. 5.7e-23;
Matches 69; Conservative 37; Mismatches 69;
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US-10-436-523-79
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Sequence 76, Application US/10436523
Fubblication No. US20030180888A1
GENERAL INFORMATION:
TITLE OF INVERTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
TITLE OF INVERTION CD2000 AND CD2001 MOLECULES, AND USES THEREOF
TITLE OF INVERTION UNMBER: US/10/436,523
CURRENT APPLICATION NUMBER: US/10/007,303
FRIOR FILING DATE: 2001-11-20
FRIOR PILING DATE: 2001-11-20
FRIOR APPLICATION NUMBER: 09/706,167
FRIOR APPLICATION NUMBER: 09/706,167
FRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                             APPLICANT: DESCRIPTION APPLICANT: APPLICANT: LADP, Hilmar APPLICANT: LADP, Hilmar APPLICANT: LADP, Hilmar APPLICANT: LADP, Hilmar APPLICANT: Kalthoff, Frank Stephan TITLE OF INVENTION: Organic Compounds FILE REFERENCE: 131347 PCT CURRENT APPLICATION NUMBER: US 60/192,934 PRIOR PILING DATE: 2000-09-06 CURRENT FILING DATE: 2000-09-06 PRIOR FILING DATE: 2000-05-18 PRIOR FILING DATE: 2000-05-18 PRIOR FILING DATE: 2000-05-18 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PRIOR FILING DATE: 2000-05-19 PR
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No. US20030124575/
No. US2003012457/
Phares, William
Werner, Gudrun
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
US-10-220-946-18
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US-10-436-523-76
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LENGTH: 289
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32.0%; Score 332; DB 14; Length 289;

Query Match

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February 4, 2005, 12:03:57; Search time 19.2216 Seconds (without alignments) 996.126 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

	Description	Ly-9.2 antigen - m		m		biliary glycoprote	biliary glycoprote	biliary glycoprote	carcinoembryonic a	biliary glycoprote	nonspecific cross-	limbic-system-asso	biliary glycoprote	biliary glycoprote	biliary glycoprote	transmembrane carc	biliary glycoprote	opioid-binding pro		opioid-binding pro	opioid-binding cel	50K glycoprotein p	neurotrimin - rat	carcinoembryonic a	T-cell surface gly	cell-adhesion mole	T-cell surface gly	pregnancy-specific	поеп	gene 2B4 protein -
SUMMARIES		A46500	801299	JL0143	258892	WMMSR1	JC1508	S34338	A36319	JC1509	A27681	JC4776	JH0395	JH0396	JH0394	C30127	A32164	JC1238	803199	JC1239	JC4025	JC5519	I56551	A55811	S41638	823969	RWHUC2	JC4123	348	149443
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	* Query Match Length	629	240	240	335	458	521	521	702	458	344	338	321	351	417	464	526	338	345	345	345	338	344	265	347	458	351	419	349	398
	* Query Match	28.4	16.7	15.9	15.4	13.4	13.4	13.1	13.0	12.7	12.7	12.0	11.8	11.8	11.8	11.8	11.8	11.7	11.7	11.7	11.6	11.5	11.5	11.4	11.4	11.1	10.9	10.9	10.6	10.6
	Score	295	174	165.5	160	139	139	136	135.5	132	131.5	125	122.5	122.5	122.5	122.5	122.5	121.5	121.5	121.5	120.5	119.5	119	118	118	115.5	113.5	113.5	110.5	110
	Result No.		8	٣	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59

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JC4024	146266	A28333	A53244	S68177	A44783	T43027	A28277	A33258	B33258	138346	PN0568	T42633	G43354	F43354	A43354
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	4.0	10.3	10.3	10.3	10.3	10.3	10.1	10.1	10.1	10.1	6.6	6.6	8.6	9.8	

ALIGNMENTS

A46500 Ly-9.2 antigen - mouse Cypecies: Mus musculus (house mouse) Cypecies: Mus musculus (house mouse) Cypecies: Mus musculus (house mouse) Cypecies: Mus musculus (house mouse) Cypecies: Mus musculus (house) Cypecies: Mus musculus (house) Cypecies: Musculus (hous
Query Match 28.4%; Score 295; DB 2; Length 629; Best Local Similarity 34.9%; Pred. No. 6.1e-17; Matches 67; Conservative 31; Mismatches 88; Indels 6; Gaps 1;
Qy 7 TVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAXVTPGDSETAPVVTVTHRNYYERIHA 66
Qy 67 LGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNS 126 : : : : : : : : :
QY 127 TCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
Oy 181 NSDSISARQLCA 192
RESULT 2 SO1299 OX 45 membrane glycoprotein precursor - rat NyAlternate names: MRC OX-45 antigen NyAlternate names: MRC OX-45 antigen C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004 C;Accession: S01299 R;Killeen, N.; Mosesner, R.; Arvieux, J.; Willis, A.; Williams, A.F. EMBO J. 7, 3087-3091, 1988 EMBO J. 7, 3087-3091, 1988 EMBO J. 7, 3087-3091, 1989 EMBC OX-45 antigen of rat leukocytes and endothelium is in a subset of the A;Reference number: S01299; MUID:89030603; PMID:3181129

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Conservative
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Best Local Similarity
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A;Reference number: J10143; MUD:90278362; PMID:1693656
A;Accession: J10143
A;Accession: J10143
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A;Accession: J10143
A;Accession: J10143
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A;Residues: 1-240 «KIL»

A;Cross-references: UNIPROT:P10252; EMBL:X13016; NID:956804; PIDN:CAA31438.1; PID:956805

A;Cross-references: UNIPROT:P10252; EMBL:X13016; NID:956804; PIDN:CAA31438.1; PID:956805

C;Superfamily: Bs—cell surface glycoprotein blast.1

C;Keywords: 91ycoprotein; membrane protein; surface antigen

F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-240/Product: OX-45 membrane glycoprotein #status predicted <MAT>
F;38,97,140,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse BCM1 (OX45 or Blast-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNYYERIHALGPNYNLVISDLRMEDAGD-YKADINTQADPYTTTKRYNLQIYRRLGKPKI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQSLMASVNSTCNVTLICSVEKEEKNVTYNW-----SPLGEEGNVLQIFQTPEDQELTY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 KIEKTKNLTDSCHIRLSCKV--BDQGVDYTWYEDSGPFPQRNPGYVLEITITPHNKSTFY 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NyAlternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0143; S21319; A47469; B47469
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
J. Exp. Med. 171, 2115-2130, 1990
A;Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 ox
                                                                                                                                                                                                                                                                                                                                                                                               1 KDSEIFTVNGILGESVTFPVNIQEPROVKIIAW---TSKTSVAYVTPGDSETAPVVTVTH 57
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                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                 16.7%; Score 174; DB 2; Length 240;
.larity 26.2%; Pred. No. 2.6e-07;
Conservative 36; Mismatches 86; Indels
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F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-217/Product: antigna BCM1 #status predicted <WAT>
F;218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F;32,38,70,136,186,203/Binding site: carbobydrate (Asn) (covalent) #status predicted
F;217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
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                                                                                                                                                                                                                                        N;Alternate names: carcinoembryonic antigen mmCGMla; murine hepatitis virus receptor C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: JCI505; A49006; A41563; S11626; S11625
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
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NDTVYFTLPC-DLA 215
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Matches 50; Conservative
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A,Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A,Reference number: JC1505, MUID:9327328; PMID:8500759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,MOJECULE LYPE: MRNA
A,Residues: 1-521 <MCS-
A,Residues: 1-521 <MCS-
A,Cross-references: UNIPROT: P31809; EMBL:X67279; NID:g50170; PIDN:CAA47696.1; PID:g50171
A,Experimental source: strain CD1; tissue colon
R,Nedellec, P.; Turbide, C.; Beauchemin, N.
R,Nedellec, P.; Turbide, C.; Beauchemin, N.
A,Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
A,Reference number: S65939; MUID:95354678; PMID:7628460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: BNBL:X84054; NID:g1039337
A;Experimental source: strain BALB/c
A;Experimental source: strain BALB/c
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A;Note: the nucleotide sequence is given
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534338
biliary glycoprotein F - mouse
biliary glycoprotein F - mouse
biliary glycoprotein
NyAlternate names: mouse hepatitis virus (MHV) receptor glycoprotein
Sybecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Musculus (forts)
C;Accession: S34338; JC1510; A41093
C;Accession: S34338; JC1510; A41093
R;Huang, X:F; Novel, M.; Novel, G.
Submitted to the EMBL Data Library, July 1992
A;Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A;Reference number: S34338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Superfamily: carcinoembryonic transmembrane protein
C;Keywords: glycoprotein; receptor; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IRMI>
F;224-303/Domain: immunoglobulin homology <IRMI>
F;339-396/Domain: immunoglobulin homology <IRMI>
F;71,89;104,148,199,206,210,226,258,290,294;304,317,333,375/Binding site: carbohydrate
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C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JGISO8; S65940; $358852
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
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Best Local Similarity 27.49
Matches 49; Conservative
                                                       D - mouse
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A; Residues: 1-458 eMC2>
A; Residues: 1-458 eMC2>
A; Residues: 1-458 eMC2>
A; Residues: 1-458 eMC2>
A; Cross-references: GBX-X15351; NID:g53020; PIDN:CAA33409.1; PID:g53021
A; Accession: G.S.; Pensiero, M.N.; Cardellichio, C.B.; Williams, R.K.; Jiang, G.S.; Holme
J. Virol. 65, 6801-6801, 1991
A; Title: Cloning of the mouse hepatitis virus (MHV) receptor: expression in human and ha
A; Reference number: A41563; MUID:92046352; PMID:1719235
A; Accession: A41563
A; Residues: 1-458 eVUE>
A; Residues: 1-458 eVUE>
A; Residues: 1-458 eVUE>
A; Reference number: S1626
A; Accession: S1626
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A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprd A;Reference number: JC1505; MUID:93273228; PMID:8500759 A;Accession: JC1505 A;Accession: JC1505 A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-458 <MCC>
A;Crosteriores: 1-658 <MCC>
A;Ccualg, K.; Turbide, C.; Beauchemin, N.
Cell Growth Differ. 3, 165-174, 1992
A;Title: mmCGMlai a mouse carcinoembryonic antigen gene family member, generated by alte
A;Reference number: A49006; MUID:92338096; PMID:1633107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Beauchemin, N.; Turbuiated, C.; Afar, D.; Bell, J.; Raymond, M.; Stanners, C.P.; Fuks, Cancer Res. 49, 2017-2021, 1984
Cancer Res. 49, 2017-2021, 1984
A;Title: A mouse analogue of the human carcinoembryonic antigen.
A;Reference number: S11625, MUID:89195121; PMID:2702644
A;Reference number: S11625
A;Accession: S11625
A;Molecule type: mRNA
A;Residues: 'PQ', 82-321 <BB2.
A;Accesser-references: EMBL:X15351
C;Comment: This protein is expressed at the cell surface and plays a determinant role: C;Comment: This protein is expressed at the cell surface and plays a determinant role:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 EDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEE 140
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Best Local Similarity
Matches 49; Conserv
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A;Status: preliminary A;Molecule type: mRNA A;Molecule type: L.2. AUNA A;Rosiduces: 1-52. AUNA A;Cross-references: UNIPROT:Q61352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g312 R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

A; Accession: S34338

----EGN-VLQIFQTPEDQELTYTCTAQNPVS-NNSDSIS 186

141 KNVTYNWSPLGE-

174 DNINYLWSRNGESLSEGDRLKLSEGNRTLTLLNVTRNDTGPYVČETRNPVSVNRSDPFS 232

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Mon Feb

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A;Gene: GDB:CEA
A;Cross-references: GDB:119054; OMIM:114890
                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA; Residues: 5-702 <OIK>
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NyAlternate names: CEA; meconium antigen 100
Cippedes: Homo sapatens (man)
Cippedes: Homo sapatens (man)
Cippedes: Homo sapatens (man)
Cippedes: Homo sapatens (man)
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Cippedes: Homo sapatens (man)
Cippedes: Homo sapatens (man)
Nol. Cell. Biol. 10, 2738-2748, 1990
A;Reference number: A36319; MUID: 90258861; PMID: 2342461
A;Reference number: A36319; MUID: 90258861; PMID: 2342461
A;Reference number: A36319; MUID: 90258861; PMID: 3424461
A;Residues: 1-702 -8CA
A;Residues: UNIPROT: P06731; GB: M17303; NID: 9178676; PIDN: AABESSS13.1; PID: 9178677
A;Residues: UNIPROT: P06731; GB: M17303; NID: 9178676; PIDN: AABESSS13.1; PID: 9178677
A;Residues: Los Couranger, D.; Puks, A.; Stanners, C.P.
Mol. Cell. Biol. 7, 3221-3230, 1987
A;Reference number: A27773; MUID: 918038876; PMID: 3670312
A;Residues: 1-702 -8EA>
A;Residues: 1-702 -8EA>
A;Residues: 1-702 -8EBA
A;Residues: 1-702 -8EBA
A;Residues: 1-702 -8EBA
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                of mouse colon biliary glycopro
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                                                                                                                                                                                                                                                                                                                                                                                                                             the carcinoembryonic antigen
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F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal h
F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site:
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A;Title: Expression of the Bgp gene and characterization A;Reference number: JC1505; MUID:93273228; PMID:8500759 A;Accession: JC1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 35-59 <WIL>
C;Comment: This protein is expressed at the cell surface
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                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-81, 'Q', 83-141, 'P', 143-521 <MCC>
A; Residues: 1-81, 'Q', 83-141, 'P', 143-521 <MCC>
A; Cross references: Gs. K767281
R; Williams, R. K.; Jiang, G. S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A; Teles Receptor for mouse hepatitis virus is a member of the second
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C,Superfamily: carcinoembryonic
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Best Local Similarity 26.8*
Matches 48; Conservative
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A;Molecule type: mRNA
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(CEA) deduced from cDNA seq
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A,Residues: 'X',140-151,'X',153,'X',155-156 <THO>
A,Residues: 'X',140-151,'X',140-151,'X',155-156 <THO>
A,ROCET this is the amino terminal end of a fragment shown to mediate uptake by Kupffer C,Comment: This heavily glycosylated membane protein of unknown function is a widely use C,Comment: This protein may be processed at its C-terminus. It is anchored to the membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinoem
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R;Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A;Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon A;Reference number: I59098; MUID:87204247; PMID:3033671
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Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoemba A;Reference number: A44476, MUID:93052339; PMID:1427854
A;Accession: A44476
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R;Siepen, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wagener, C.
B;Ophys. Res. Commun. 147, 212-218, 1987
A;Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and A;Reference number: A26831; MUID:87326349; PMID:3632664
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A;Residues: 35-64 <SIE>
R;Thomas, P.; Toth, C.A.
Biochem. Biophys. Res. Commun. 170, 391-396, 1990
A;Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located
A;Reference number: A35490; MUID:90321257; PMID:2372297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 35-141 <KHA>
R; Willicocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A; Title: Characterization of the genomic organization of human carcinoembryonic
A; Reference number: I54224; MUID: 91139118; PMID: 2286372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Wolecule type: mRNA
A; Residues: 5-319, 321-702 <012>
A; Cross-references: EMBL:X16455; NID:g29854; PIDN:CAA34474.1; PID:g825638
R; Barnett, T.
submitted to the EMBL Data Library, September 1991
A; Description: Genomic DNA sequence upstream of the translational start of the of
A; Reference number: S31737
A; Accession: S31737
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-141 < BA2>
A; Cross-references: EMBL:X62151
                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GB:M15042; NID:g180198; PIDN:AAA51963.1; PID:g180199
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A;Residues: 1-702 <BAR>
A;Cross-references: GB:M29540; NID:g180222; PIDN:AAA51967.1; A;Note: the authors translated the codon GTG for residue 130 of R;Oikawa, S.; Nakazato, H.; Kosaki, GBiochem, Biophys. Res. Commun. 142, 511-518, 1987
A;Title: Primary structure of human carcinoembryonic antigen A;Reference number: A25845; MUID:87128144; PMID:3814146
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rjoikawa, S.
submitted to the EMBL Data Library, September 1989
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A;Noclecule type: mRNA
A;Residues: 311-702 <RE2>
A;Cross-references: GB:M16234; NID:g180240;
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A;Molecule type: DNA
A;Residues: 1-37 <RES>
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A;Accession: S08106
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A,Molecule type: mRNA
A,Residues: 1-458 <MCC.
A,Cross-references: UNIPROT:Q61351; GB:X67280
C,Comment: This protein is expressed at the cell surface and plays a determinant role in C,Genetics:
A;Map position: 19q13.2-19q13.2
A;Map position: 19q13.2-19q13.2
A;Introns: 22/1; 42/1; 326/1; 326/1; 438/1; 591/1; 676/1
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin c;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat; F;1-134/Domain: carcinoembryonic antigen precursor amino-terminal homology cCEAN> F;1-34/Domain: signal sequence #status predicted cASI>
F;1-34/Domain: signal sequence #status predicted cASI>
F;1-67/Product: carcinoembryonic antigen #status predicted cAMI>
F;160-217/Domain: immunoglobulin homology cIMM1>
F;252-301/Domain: immunoglobulin homology cIMM3>
F;516-573/Domain: immunoglobulin homology cIMM3>
F;516-573/Domain: immunoglobulin homology cIMM5>
F;608-657/Domain: immunoglobulin homology cIMM5>
F;608-657/Domain: carboxyl-terminal propeptide #status predicted cCTP>
F;679-702/Domain: carboxyl-terminal propeptide #status predicted carboxyl cin mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: JCL509
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Bene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopromates. Expression of the Bgp gene and characterization of mouse colon biliary glycopromaterence number: JCL505; MUID:93273228; PMID:8500759
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C,Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
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F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;16-219/Domain: immunoglobulin homology <IMM1>
F;264-303/Domain: immunoglobulin homology <IMM2>
F;384-306/Domain: immunoglobulin homology <IMM3>
F;387-396/Domain: immunoglobulin homology <IMM3>
F;387-306/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEE 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SP---LGEEGNV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 PELPKPSISSNNSKPVEDKDAVAFTC--EPETQDATYLWWVNNQSLPVSPRLQLSNGNRT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biliary glycoprotein E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb_1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVNIQEPRQVKII-----TPGDSETAPVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLFNVTRNDTASYKCETONPVSARRSDSV 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.0%;
Query Match
Best Local Similarity 24.3%;
Matches 51; Conservative
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Best Local (
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nonspecific cross-reacting antigen precursor - human
NyAlternate names: NCA; TEX/NCA
C;Species: Homo sapiens (man)
C;Dates: Homo sapiens (man)
C;Dates: J-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C;Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F47
C;Accession: A26902; A29875; A7781; B31037; A29918; A27709; A36271; C26414; E44476; F47
B;Ochem. Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A;Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) generate number: A26902; MUID:87298464; PMID:3619891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A28875
A; Accession: A28875
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A; Residues: 1-238, V', 240-344 <TAW>
A; Residues: 1-238, V', 240-344 <TAW>
A; Residues: 1-238, V', 240-344 <TAW>
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A; Cross-references: GE:M18728; NID:g189084; PIDN:AAAS9907.1; PID:g189085
B; Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A; Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and A; Reference number: A3037; MUD:88139389; PMID:320478
A; Residues: 1-137, L', 139-344 <BAR>
A; Residues: 1-137, L', 139-344 <BAR>
A; Residues: 1-137, L', 139-344 <BAR>
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A; Residues: 1-137, L', 139-344 (BAR>
A; Residues: 1-137, L', 139-344 (BAR>
A; Residues: 1-137, L', 1988
A; Note: the authors translated the codon TTG for residue 138 as Phe
B; Neumaier, M.; Zimmermann W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
A; Neumaier, M.; Zimmermann G. CDNA clone for the nonspecific cross-reacting antigen (Nr A; Reference number: A29918; MUD:88139389; PMID:2830274
A; Accession: A29918
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A; Residues: 1-34 < NEUS.
A; Residues: 1-34 < NEUS.
A; Cross-references: GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51739.1; PID:g178691
A; Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
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A; Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and in.
A; Reference number: A27709; MUID:88268882; PMID:3390172
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A;Residues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-23
R;Hefte, S.A.; Paxton, R.J.; Shlavely, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A;Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspec
A;Reference number: A36271; MUID:90256782; PMID:2341397
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A;Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194,204-224;233-308;31
R;Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation A;Reference number: A26414; MUID:87147209; PMID:3469650
EGN-VLOIFOTPEDQELTYTCTAQNPVS-NNSDSIS 186
                                                                                     KNVTYNWSPLGE
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biliary glycoprotein i precursor - human C; Species: Homo sapiens (man)
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A;Map position: 19913.2-19913.2
A;Map position: 19913.2-19913.2
A;Introns: 22/1
A;Note: the list of introns may be incomplete
G;Superfamily: carcinoembryonic antigen; carcinoembryonic inpoprotein; membrane protein; phosphati
F;1-38/Domain: carcinoembryonic antigen precursor amino-termin
F;1-38/Domain: signal sequence #status predicted <SIG>F;1-34/Domain: immunoglobulin homology <IMMI>F;222-301/Domain: immunoglobuli
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A;Gene: lamp
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
                                                                                                                                                                                                                       estimation|of the size of the carcinoemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalent F;309/Binding site: carbohydrate (Asn) (covalent) #status predicted F;320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form
                                                                                                                     ς.
A; Residues: 35-69 cPAX>
R; Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S. Genomics 14, 384-390, 1992
Genomics 14, 384-390, 1992
A; Title: Identification of three new genes and estimation of the size of the carcinoemt A; Reference number: A44476; MUID:93052339; PMID:1427854
A; Accession: E44476
A; Accession: E44476
A; Residues: 35-141 cKHA>
A; Residues: 35-141 cKHA>
A; Residues: 35-141 cKHA>
A; Retue: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 35-137, L', 139-141 cKH2>
C; Comment: This protein appears to be processed at the carboxyl terminus and anchored to contain the contains and anchored to contain the contains and anchored to contain the contains and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and anchored to contain the carboxyl terminus and contain the carboxyl terminus and anchored to contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carboxyl terminus and contain the carbox
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C;Species: Homo sapiens (man)
C;Date: 10-May_1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
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C; Keywords: brain, glycoprotein; membrane protein; phosphoprotein
F;1-7/Domain: signal sequence #status predicted <SIG>
F;1-3/Abegion: hydrophobic
F;40, 66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status pred
F;42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predicted
F;95,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biliary glycoprotein h precursor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0395
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones frankacesnoc number: JH0394; MUID:9122218; PMID:205273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/MOLECULE TYPE: MRNA
A/RESIGUES: 1-31 «KUR»
A/RESIGUES: 1-31 «KUR»
A/RESIGUES: 1-31 «KUR»
A/Cross-references: UNIPROT:P13689, GB:M69176; NID:g179434; PIDN:AAA51825.1; PID:g179435.
A/Cross-references: UNIPROT:P13689, GB:M69176; NID:g179434; PIDN:AAA51825.1; PID:g179435.
A/Cross-references: Telekocyte
C/Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C/Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-termin.
F/1-134/Domain: carcinoembryonic antigen precursor amino-terminal homology cCEAN>
F/35-321/Product: biliary glycoprotein h #status predicted cAIG>
F/35-321/Product: biliary glycoprotein h #status predicted cAIT>
F/160-217/Domain: immunoglobulin homology cIMM1>
F/252-301/Domain: immunoglobulin homology cIMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 VAWLNRSGIIFAGHDKWSLDPRVEL-----EKRHSL--EYSLRIQKVDVYDEGSYTCSV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 NTQADPYTTTKRYNLQIYRRLGKPKITQ-SLMASVNSTCNVTLTCSVE-KEEKNVTY-NW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 IAWISKISVAYVIPGDSETAPVVIVIHRNYYERIHALGPNYNLVISDLRMEDAGDYKADI
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                                                                                                                                                                                                                                                                          Length 338;
                                                                                                                                                                                                                                                                                                                                                      67; Indels
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11.8%; Score 122.5; DB 2;
Best Local Similarity 24.4%; Pred. No. 0.0081;
Matches 52; Conservative 31; Mismatches 65;
                                                                                                                                                                                                                                                                      Score 125; DB 2;
Pred. No. 0.0053;
27; Mismatches 67,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTGREFEGEEEYLEILGITREOSGKYECKAANEVSS
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1 Similarity 27.4%;
43; Conservative 2
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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transmembrane carcinoembryonic antigen 3 precursor - human
N.Alternate names: CD66 splice form BGPc
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: C30127; 152597
R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; F,Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; F,Astrie: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNA
A;Recension: C30127.
A;Accession: C30127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-646 cBAR>
A; Residues: 1-646 cBAR>
A; Cross-references: UNIPROT:Q16170; EMBL:X16356; EMBL:X14784
B; Cross-references: UNIPROT:Q16170; EMBL:X16356; EMBL:X14784
R; Watt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Gschmeissner, S.E.; Hajibagher
Blood 84, 200-210, 1994
A; Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, exp.
A; Reference number: 152597; MUID:94289702; PMID:8018919
A; Accession: 152597
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-464 < RES5,
A; Cross-references: GB:S71326; NID:g550030; PIDN:AAB31183.1; PID:g550031
A; Cross-references: GB:S71326; NID:g550030; PIDN:AAB31183.1; PID:g550031
C; Cross-references: GB:S71326; NID:g550030; CS:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor antigen; transmembrane protein C; Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein C; Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein F; 1-134 Domain: carcinoembryonic antigen antigen 3 #status predicted <MAT>
F; 1-34 Domain: immunoglobulin homology < IMM1>
F; 252-301/Domain: immunoglobulin homology < IMM3>
F; 341-398 Domain: immunoglobulin homology < IMM3>
F; 424-455 Domain: transmembrane #status predicted < TMM>
F; 424-455 Domain: transmembrane #status predicted < TMM>
F; 424-455 Domain: transmembrane #status predicted < TMM>
F; 424-455 Domain: transmembrane #status predicted < TMM>
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F; 424-455 Domain
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                                                                                                                                                                                                                                               17 TFPVNIQEPRQVKII------AW-----TSKTSVAY-----VTPGDSETAPV 52
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                                          VIVIHRNYYERIHALGPNYNLVISDLRMEDAGDY--
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Matches 52; Conserv
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A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr A;Reference number: JH0394, MUID:91222218; PMID:2025273
A;Reference number: JH0394
A;Rocession: JH0394
A;Rocession: JH0394
A;Rocession: JH0394
A;Rocession: JH0394
A;Residues type: mRNA
A;Residues type: mRNA
A;Residues: 1-417 cUNP.
A;Cross-references: UNIPROT:P13688; GB:M72238; NID:g179436; PIDN:AAA58394.1; PID:g179438
A;Experimental source: leukocycte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-termin F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology cCAN>
F;1-34/Domain: signal sequence #status predicted <SIG>F;35-333/Product: biliary glycoprotein g #status predicted <MAT>F;160-217/Domain: immunoglobulin homology <IMM1>F;25-301/Domain: immunoglobulin homology <IMM3>
F;341-338/Domain: immunoglobulin homology <IMM3>
                                  Circlesion: J40396
Rikuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem: Biophys. Res. Commun. 176, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
A; Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A; Reference number: J40394; MulD:9122218; PMID:2025273
A; Reference number: J40394; MulD:9122218; PMID:2025273
A; Residues: 1-351 «KUR»
A; Residues: 1-351 «KUR»
A; Residues: 1-351 «KUR»
A; Residues: 1-351 «KUR»
A; Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C; Comment: Biliary glycoproteins belong to the carcinoembryonic antigen precursor amino-termin C; Keywords: glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane protein
F; 1-134 Domain: aarcinoembryonic antigen precursor amino-terminal homology cEAN»
F; 1-34 Domain: immunoglobulin homology cIMM1>
F; 252-301/Domain: immunoglobulin homology cIMM2>
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
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11.8%; Score 122.5; DB 2;
Best Local Similarity 24.4%; Pred. No. 0.009;
Matches 52; Conservative 31; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVLQIFQTPEDQELTYTCTAQNPVS-NNSDSIS 186
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.larity 24.4%; Pred. No. 0.011;
Conservative 31; Mismatches 6
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Sequence:

Title: Perfect

Run on:

Searched:

Database

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MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Best Local Similarity 100.0%; Score 1039; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 199; Conservative 0; Mismatches 0; Indels 0
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Palou E., Gold J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, FAFO34817; AAF21723.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-11ke.
SMART; SM00409; IG; 1.
PROSTIE; PROS1055; IG LIKE; 1.
SEQUENCE 272 AA; 30514 MW; 6A2E13AA4E22E13E CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD84d.
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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LY9 HUMAN
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1: uniprot_sprot:*
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MEDINE-1978 PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MISCHINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausher R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,

A Alschul S.E., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsiath F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muray D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Soung A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Maring M., Marra M.A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. Mederzation and initial analysis of more than 15,000 full-length human
                                                121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                                                                                                                                                                                                                                                                     01-JAN.1998 (TrEMBLrel. 05, Created)
01-JAN.1998 (TrEMBLrel. 05, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Leukcoyte antigen CD84 (Leukcoyte differentiation antigen CD84 (softorm CD84) (MAX.3 cell surface antigen precursor) (CD84 antigen).
                                                                     MEDLINE-86188202; PubMed=3008886; Andreesen R., Bross K.J., Osterholz J., Emmrich F.; "Human marrophage maturation and heterogeneity: analysis with a newly generated set of monoclonal antibodies to differentiation antigens."; Blood 67:1257-1264(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                            nomo approme nument.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20164057; PubMed=10698700; DOI=10.1042/0264-6021:3460729; Krause S.W., Rehli M., Heinz S., Ebner R., Andreesen R.; "Characterization of WAX.3 antigen, a glycoprotein expressed on macrophages, dendritic cells and blood platelets: identity with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97454416; PubMed=9310491;
de la Frente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
"CD84 leukocyte antigen is a new member of the Ig superfamily.";
Blood 90:2398-2405(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palou E., Sole J., Pirotto F., Gaya A., Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                       328 AA
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                                                                                                                                                       202 NSDSISARQLCADIAMGFR 220
                                                                                                                                199
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                                                                                                                                NSDSISARQLCADIAMGFR
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                                                                                                                                                                                                                                                                                        O15430; Q8WLP1;
                                                                                                                                                                                                                                                                                                                                                                                                            Name=CD84;
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                                                                                        SEQUENCE FROM N.A.
Palou B., Freed J.H., Sole J., Pi A., Vilella A., Vives J., Gaya A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
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bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
(CEI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
Korn B., Zuo D., Hu Y., LaBaer J.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
ENBL, CR541847; CAG46645.1; -.
InterPro; IFR003599; IG.
InterPro; IFR003199; IG.
SMART; SM00409; IG; 2.
PROSITE; PSS0835; IG_LIKE; 1.
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Last annotation update)
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100.0%; Pred. No. 1.9e-82;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.5e-82;
ive 0; Mismatches 0;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity 100.
Matches 199; Conservative
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Name=CD84;
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                                           MASYNSTCNVTLTCSVEKEEKAVTYNWSPLGEGAVLQIFGTFEDGELTYTCTAQNPVSN 180
                                                                                                                                                    142 MASVNSTCNVTLTCSVEKEERNVTXNWSPLGEEGNVLQIFQTFEDQELTYTCTAQNPVSN 201
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            YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 2e-82;
Matches 199; Conservative 0; Mismatches 0; Indels
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, ARC54016; AAF21722.1; -.
Genew, HGNC:1104; CDB4.
InterPro; IPR0013599; IG.
InterPro; IPR001110; Ig-11ke.
SMART; SM00409; IG. II.KE: 1.
SRONITE; PRS0035; IG LIKE; 1.
SEQUENCE 345 AA; 38782 MW; DA06BC5A682E62DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UIB8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD84a.
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(1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte antigen CD84 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OL-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 26, Chordata, Craniata, Vertebrata, Euteleostomi;
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (TrEMBLrel. 26, Chordate)
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10-OCT-2003 (TrEMBLrel. 26, Chordate)
10-OCT-2003 (Tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 328;
                                                                       A Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; U82988; AAR84364.1; --
R EMBL; AA223324; AAF21721.1; --
R EMBL; AA223324; CAA11264.1; --
R EMBL; BCC20063; AA420063.1; --
R EMBL; BCC20063; AA420063.1; --
R GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0005987; C:integral to plasma membrane; TAS.
R GO; GO:0007156; P:defense response; TAS.
R GO; GO:0007110; Ig-like.
R InterPro; IPR007110; Ig-like.
R SMART; SM00409; IG; 1.
R PROSITE; PS50835; IG_LIKE; 1.
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Submitted (APR.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y12632; CAA73181.1; -.
SWART; SMOGHOS; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAX.3 cell surface antigen.; 6C9A89206A6D0344 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1039; DB 2;
100.0%; Pred. No. 1.9e-82;
tive 0; Mismatches 0;
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22 328 MA
328 AA; 36871 MW;
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Matches 199; Conservative
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Matches 199; Conservative
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                        SEQUENCE FROM N.A.
TISSUE=Lymph;
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Q8WWI8;
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SIGNAL
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142 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 201
       82 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 KGRIEIIDQKYDLVIRDLRMEDAGTYKADINEENEE-TITKIYYLHIYRRLKTPKITQSL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                   MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Engel P.;
"Molecular cloning, characterization, and chromosomal localization of the mouse homologue of CD84, a member of the CD2 family of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 KDADPUVMNGILGESVTFLLNIQEPKKIDNIAWTSQSSVAFIKPGVNKAE--VTITQGTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Cd84; Synonyms=CD84;
Nus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LY9 HUMAN STANDARD; PRT, 655 AA. 09HBG7; 014775; Q9HBG7; Q9NQ24; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) 05-UUL-2004 (Rel. 44, Last annotation update) (Cell-surface antigen Ly-9) (CD229 antigen). Name=LY9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB=Peritoneum;
MEDLINE=99180614; PubMed=10079287; DOI=10.1007/8002510050490;
de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uniface molecules.",

Immunogenetics 49:249-255(1999).

EMBL; AF043445, AB002273.1; -.

MGD; MGI:1336885, Cd84.

InterPro; IPR003599; Ig.

InterPro; IPR007110; Ig-like.

SMART; SM00409; Ig! Like; 1.

PROSITE; PSS0835; IG Like; 1.

SEQUENCE 329 AA; 37345 MW; 43BBIAASAF1989E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) CD84 leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duery Match 58.8%; Score 610.5; DB 2; Best Local Similarity 61.7%; Pred. No. 5e-45; Matches 119; Conservative 32; Mismatches 39;
                                                                                                                                                                                                                                                                                                    329 AA.
                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                       181 NSDSISARQLCA 192
                                                                                                                                                                               NSDSISAROLCA 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                              01-MAY-1999
                                                 121
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Q9Z178;
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Q9Z178
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ID LY9 H
AC 09HBG
DT 28-FE
DT 28-FE
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DE T-1ym
GR Name=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLGIYRRLGKPKITQSL 120
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           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palou E., Sole J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF054018; AAF21724.1; -.
InterPro; IPR003599; Ig.
InterPro; IRR007110; Ig-like.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                  197 197
197 AA; 21889 MW; 2E660BF5FA871D88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG_LIKE, 1.
; Z6902 MW; F0121BC1609B6C52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD84s.
                                                                                                                                                                                                                                                                                                                                                                                                 96.5%; Score 1003; DB 2;
ilarity 100.0%; Pred. No. 1.4e-79;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AA
                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSDSISAROLCA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSDSISAROLCA 197
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Best Local Similarity
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SEQUENCE 241 AA
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                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
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                                                                                                                                                                       McKenzie I.F.; "and characterization of cDNA clones for Humly9: the human "Isolation and characterization of cDNA clones for Humly9: the human homologue of mouse Ly9."; Immunogenetics 43:13-19(1996).
                                                                                                                                                                                                                                                                              ZBQUENCE OF 99-655 FROM N.A. (ISOFORM 3).
Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A., Margolin J.F.;
Margolin J.F.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May participate in adhesion reactions between T lymphocytes and accessory cells by homophilic interaction.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 600684; -.
GO; GO:0005887; C:integral to plasma membrane; ISS.
GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); NAS.
                                                         SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20424510; PubMed=10970093; DOI=10.1007/s002510000209;
Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
Torar Structure of the mouse leukocyte cell surface molecule Ly9.";
Immunogenetics 51:788-793(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=3;
IsoId=Q9HBG7-3; Sequence=VSP_002524, VSP_002525, VSP_002526;
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-lymphocyte surface antigen Ly-9. Extracellular (Potential). Potential.
                                                                                                                                                          Sandrin M.S., Henning M.M., Lo M.F., Baker B., Sutherland G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 2.
SNART; SM00409; IG; 2.
PROSITE; PS50815; IG_LIKE; 2.
Alternative splicing; Antigen; Cell adhesion; Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.
SIGNAL 1 47 Potential.
                                                                                                                                                                                                                                                        Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
19-like V-type 1.
19-like C2-type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9HBG7-2; Sequence=VSP_002525;
                                                                                                                                 SEQUENCE OF 32-654 FROM N.A. (ISOFORM 2). MEDLINE=96128248; PubMed=8537117;
                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9HBG7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF244129, AAG14995.1; -.
EMBL, L42621, AAA92623.1; -.
EMBL, AL121996; CAC00580.1; -.
EMBL, AX007142; AAG02002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR003599; Ig.
InterPro, IPR007110; Ig-like.
                                                                                                                                                                                                                                  SEQUENCE OF 1-151 FROM N.A.
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   sapiens (Human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                    (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
33.9%; Score 352; DB 1; Length 655;
Best Local Similarity 38.1%; Pred. No. 4.4e-22;
Matches 77; Conservative 41; Mismatches 70; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Zhang W., Yu M., Cao X.; Zhang W., Wan T., Li N., He L., Yuan Z., Yu M., Cao X.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                Potential.
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Missing (in isoform 3).
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2-COT-2004 (TrEMBLrel. 28, Last annotation update)
CD84-H1 (CD2 family 10) (SLAM family member 9).
Name=SLAMF9.
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Missing (in Ref. 1).
V -> M (in Ref. 4).
Ig-like V-type 2.
Ig-like C2-type 2.
Potential.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
B Grechench C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M. J. Osares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Bosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villadon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
Indense J.M. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Director MGC Project;
Submitted (UNL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275725; AAK69052.1; -.
EMBL; AF34613; AAK61991; -.
EMBL; BC074754; AAK14754.1; -.
Genew; HGNC:18430; SLAMF9.
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InterPro; IPR001559; Ig.
InterPro; IPR007110; Ig-like.
SWART; SM0409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Last sequence update)
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es 69; Conservative
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01-MAR-2004 (TrEMBLrel.
SLAM family member 9.
Name=Slamf9;
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01-MAR-2002
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SEQUENCE FROM N.A. STRAIN=FVB/N; TISSUE=Mammary tumor;

NCBI_TaxID=10090;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
R. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A plokins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Batchenko D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malke J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rabey J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 ISEEGVCNISLTCSIERAGMDVTYIWLSSQDSTNTSHEGSVLSTSWRPGDKAPSYTCRVS 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 DSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLM
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01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Mus musculus B lymphocyte B cells cRL-1702 WEHI 231 cDNA, RIKEN full-length enriched library, clone:G430073H03 product:weakly similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.6%; Score 328.5; DB 2; Length 285; 36.7%; Pred. No. 1.8e-20; Live 31; Mismatches 88; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019477; AAH19477.1; -
MDJ; MGI:1923692; Slamf9.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
SWART; SMO0409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 285 AA; 31728 MW; D84BFF8142367F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE-Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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NPVSNISSRRISVGSFCAD 220
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SEQUENCE FROM N.A.
TISSUE=B lymphocyte;
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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122 ASVNSTCNVTLTCSVEKEEKNVTYNW-----SPLGEEGNVLQIFQTPEDQELTYTCTAQ 175 ERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTIKRYNLQIYRRLGKPKITQSLM 121

DEDPEEVIGVLQESINLSLEIPSNEEIKHIDWLFQNNIAIVKPGKKGQPAVIMAVDPRYR 81

62

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193

NPVSN-NSDSISARQLCAD

176

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TISSUE FROM N.A.

TISSUE IJYMPhocyte;
A dadchi J., Alzawa T., Bono H., Carninci P.,
Adachi J., Alzawa K., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramotco K., Hiracka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Katoh H., Kawai J., Kojima Y., Myazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Tanaka T.,
A Tomaru A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Lu Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                         TISSUB-B lymphocyte;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=B lymphocyte;
MEDILME=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDILME=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE Iymphocyte;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKIS integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                    RIKEN FANTOM CONSOrtium; RIKEN FANTOM CONSORtium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.1%; Score 323.5; DB 2; Length 285; 36.2%; Pred. No. 4.8e-20; ive 31; Mismatches 89; Indels 7.
                                                                                                                                                        MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48675E0611027B3B CRC64;
                     Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; GO:0005615; C:extracellular space; TAS. 30; GO:0016021; C:integral to membrane; TAS. InterPro; IPR03599; IG. InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 285 AA; 31759 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK090041; BAC41061.1; -
                                                                                                                                                                                                                                                                                                                                                                                                            Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1923692; Slamf9
                                                                                                                                       TISSUE=B lymphocyte;
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The PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length conse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C5PBL/64; TISSUB=Tongue;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Milbata K., Itch M., Azawa K., Kitsunai T., Tashiro H., Itch M.,
Sunin N., Ishii Y., Nakamura S., Hazawa M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
STRAIN=C57BL/6J; PubMed=11217851; DOI=10.1038/35055500;
MINELINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                         enriched
14-H1 (CD2
                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enric
library, clone:2310026104 product:weakly similar to CD84-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                      285 AA.
                                                                                                                                                Created)
                                                                                                      PRT;
202 NPVSNISSHRİSVGSFCAD 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 420:563-573(2002).
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                          Name=Slamf9;
                                                                                                                                                    01-JUN-2001
                                                                                                                                                                                                                                   library, c.
                                                                                                                              090060
                                                                                                           090180
                                                                                                                                                                                                                                                         FAMILY
                                                                 RESULT 14
                                                                                                           g
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5 61

Gaps

7;

Best Local Similarity 36.2 Matches 72; Conservative

Query Match

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Exp. Med. 194:235-246(2001).
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CARBOHYD
CARBOHYD
                                                     ERRATUM.
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DOMAIN
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                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Adachi J. Aizawa K. AAAhira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., AAAhira S., Akimura T., Bukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Fakahashi F.,
Sano H., Sasaki D., Shibata K., Shibata Y., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMDJ MGI:1923692; Slamf9.
RDJ GO:0016021; C:integral to membrane; TAS.
RITEPPO: IPR003199; IG-like.
RMRT; SMOA109; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ASVNSTCNVTLICSVEKEEKNVTYNW-----SPLGEEGNVLQIFQTPEDQELTYTCTAQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 DEDPEEVVGVLQESINLSLEIPSNEEIKHIDWLFQNNIAIVKPGKKGQPAVIMAVDPRYR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSCUTANO SATIONARY)
PKRI; 332 AA.
OSCUTAL-2004 (Rel. 44, Created)
OS-JUL-2004 (Rel. 44, Last sequence update)
OS-JUL-2004 (Rel. 46, Last sequence update)
SIAM family member 6 precursor (NK-T-B-antigen) (NTB-A) (Activating NK receptor) (UNG6123/PRO20080).
Name=SIAMF6; Synonyms=KALI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., FUNCTION, PHOSPHORYLATION, TISSUE SPECIFICITY, AND INTERACTION WITH SH2DIA/SAP; PIN6 AND PIN11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "NTB-A, a novel SH2D1A-associated surface molecule contributing to the inability of natural killer cells to kill Epstein-Barr virus-infected B cells in X-linked Lymphoproliferative disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-21382389; PubMed=11489943;
Bottino C., Falco M., Parolini S., Marcenaro E., Augugliaro R., Sivori S., Landi E., Biassoni R., Notarangelo L.D., Moretta L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 285;
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 285 AA; 31764 MW; 33BDB4A633ASC1B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.9%; Score 321.5; DB 2; Best Local Similarity 35.7%; Pred. No. 7.2e-20; Matches 71; Conservative 32; Mismatches 89;
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                                                                                                                         MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Mend J., Chow B., Chini C., Crowley C., Currell B., Deuel B., Dowd P., Raton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., A Huang A., Xim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Andlen R., Wateanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;
Mescreted protein discovery initiative (GPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pubmed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
-!- FUNCTION: Triggers cytolytic activity only in natural killer cells (NK) expressing high surface densities of natural cytotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: Interacts with PTN6 and, upon phosphorylation, with PTN11 and SH2DIA/SAP.
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-!- PTM: Phosphorylated.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Bottino C., Falco M., Parolini S., Marcenaro E., Augugliaro
Sivori S., Landi E., Biassoni R., Notarangelo L.D., Moretta
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Cytoplasmic (Potential).
Ig-like.
By similarity.
N-linked (GlCNAc. ...) (Potential).
N-linked (GlCNAc. ...) (Potential).
N-linked (GlCNAc. ...) (Potential).
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Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Glyc
Phosphorylation; Receptor; Sign
SIGNAL
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Best Local Similarity 36.9%; Pred. No. 2.4e-19;
Matches 73; Conservative 43; Mismatches 69; Indels 13; Gaps
266 266 Missing (in Ref. 1, CAC59749).
332 AA; 37345 MW; 46D8141A0D198091 CRC64;
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Aal24045 Human bre Aax41382 Human sec

protein

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Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein; immune proliferative disorder; immune disorder; rheumatoid arthritis; carcinoma; autoimmune disorder; multiple sclerosals; Grave's edisease; hashimoto's disease; acquired immune deficiency syndrome; hepatotropic; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psociasis; apoptotic disorder; systemic lupus erythematosus; bronchitis; diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis; acute myeloid leukaemia; pane hemophilia; anaemia; gene therapy; cytostatic; immunosuppressive; neuroprotective; antinflammatory; Crohu's disease; osteopathic; antibacterial; immunomodulator; inflammatory bowel disease; jaundice; dermatological; ulcerative colitis; AlbS; CD84; gene; de
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/product= "Human CD84 protein"
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                                                     ADQ23399
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                                                                                                                                                                                                                                                                                                                                 Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a condition that benefits from modulating regulatory or effector T cell function comprises administering an agent that modulates the expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbetal, Jagged-1 or GPR-32).
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                                                                                                                                                     09-OCT-2002; 2002US-0417102P.
09-OCT-2002; 2002US-0417103P.
09-OCT-2002; 2002US-0417243P.
18-OCT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0424777P.
08-NOV-2002; 2002US-0424881P.
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                                                                                                                                                                                                                                         which comprises obtaining a lirst soft tissue sample from an individual and a normal soft tissue sample from the same or different individual determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated but of the invention. The current sequence is that of a human soft tissue sarcoma upregulated but of the invention. The current sequence is that of a shown within the
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                                                                                                    Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GGAAAAGACTCAGAAATCTTCACAGTGAATGGGATTCTGGGAGGGCTCAGTCACTTCCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                invention relates to a novel method for detecting soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;
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(PROT-) PROTEIN DESIGN LABS INC
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GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAAGAGAGGGGTAATGTCCTTCAAATC
                                                               AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg
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                                             610 Trccagacrccrgaggaccaagagcrgacrracacgrgracagcccagaacccrgrcagc
                                                                                               AACAATTCTGACTCCATCTCTGCCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT
                                                                                                                                                                    SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein gene 164 clone HSAWF26.
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Greene JM;
                                                                                                                                                           Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                                                                                                           Claim 1; Page 402-404; 721pp; English.
      9703-0056889P
9703-0056892P
9703-0056893P
9703-0056903P
9703-0056908P
9703-0056910P
9703-0056911P
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P-PSDB; AAW74891.
                                 22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
05-SEP-1997;
                                                                                                05-SEP-1997;
05-SEP-1997;
12-SEP-1997;
02-OCT-1997;
                 22-AUG-1997;
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This sequence represents a nucleic acid molecule designated Gene 164 from the human cDNA clone HSAMF26 (deposited as clone ATCC 97903 and ATCC 209049) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-075912; amino acid sequences AAW74731-WY5050 which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polypurcleotides.

Specific uses are described for each of the 186 polynucleotides, based on which lissues they are most highly expressed in (see AAV59511 for described uses)

U; 6 Other; . T; 0 G; 772 712 Sequence 3173 BP; 910 A; 773 C;

		20	110	40	170	9	23(
3173 328 0 0 0	,	1 MetalaGlnHisHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaala 20	Arddercaecaecerarddarerraererraeceraeaaaecraecaeaaacaaca 110	21 GlyLygAspSerGlullePheThrValAsmGlyIleLeuGlyGluSerValThrPhePro 40		41 ValAsnileGinGluProArgGlnValLysIlelleAlaTrpThrSerLysThrSerVal 60	
Length: Matches: Conservative: Mismatches: Indels: Gaps:	74 (1-3173)	olleLeuLeuLeuCysLeuGlnThr	sarctrocrerrecere	ullePheThrValAsnGlyIleLe	CACAGTGAATGGGATTCTC	GlnValLysileileAl	SCAAGTTAAAATCATTGC
2.27e-163 1695.00 100.00\$: 100.00\$ 2 9.94\$	329) x AAV5967	lnHisHisLeuTri	AGCACCACCTATG	spSerGlullePhe	ACTCAGAAATCTT	legingluProAr	TCCAAGAACCACG
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-09-882-171-483 (1-329) x AAV59674 (1-3173)	1 MetAlaG	51 Arddcrc	21 Glytysk	 111 GGAAAAG	41 ValAsnI	 171 GTAAATA
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61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80

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TyrTyrGluArg11eHisAlaLeuGlyProAsnTyrAsnLeuVal11eSerAspLeuArg
                                                                       291 TATTATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGG
                                                                                                                   MetGluaspalaglyasptyrLysAlaaspIleAsnThrGlnAlaaspProTyrThrThr
                                                                                                                                            351 ATGGAAGACGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC
                                                                                                                                                                                 ThrLysArgTyrAsnLeuGln1leTyrArgArgLeuGlyLysProLys1leThrGlnSer
                                                                                                                                                                                                       411 ACCAAGGGTACAACTIGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGT
                                                                                                                                                                                                                                                                  GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGGAGAAGAGGGTAATGTCCTTCAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                   TTCCAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg
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Ferrie AM,
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a a sequences also given in the specification. The protein is used in a a pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmum diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, pacebrovascular disorders e.g. corneal infection. The polypeptides can also be used to aid wound confluence of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, coffactors and other nutritional components. The present sequence represents a cDNA derived from a gene , Rosen CA, Fischer CL, Soppet DP, Carter KC; DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; M, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; , Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or Example 1; SEQ ID NO 174; 129pp; English.

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140 470 160 GlulysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180 200 650 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220 710 240 770 350 170 230 encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was obtained in electronic format directly from USPTO at 110 40 8 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr rcricagneriririciriccerriciaagagagagagagargcrecreaagaaaacc 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro GTAAATATCCAAGAACCACGCCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTT TyrTyrGluArg1leHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg ThrLysargTyrasnLeuGln1leTyrargArgLeuGlyLysBroLys1leThrGlnSer AlanyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn ValasnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal G; 772 T; 0 U; 6 Other; 3173 328 0 0 0 Length: Matches: Conservative: Mismatches: Indels: segdata.uspto.gov/seguence.html?DocID=6420526B1 Gaps: (1-3173)712 Ü US-09-882-171-483 (1-329) x ABS73661 2.27e-163 1695.00 100.00% 100.00% 99.94% BP; 910 A; 773 Percent Similarity: Best Local Similarity: Sequence 3173 Alignment Scores: Pred. No.: 351 411 41 61 141 471 531 181 591 201 651 221 711 241 81 101 121 Query Match: Score: g D a 유 8 유 δ ò 셤 g 셤 ð 유 à 요 ઠે ò ઠ 8888888 셤 셤 ð ઠે ò ઠે ઠે

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   Human, secreted protein, hyperproliferative disorder; leukaemia; breast cancer; wound; reproductive disorder; blood-related disorder; has breast cancer; wound; reproductive disorder; blood-related disorder; has been cancer; wound; reproductive disorder; multiple sclerosis; wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis; graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma; wiral infection; fungal infection; AIDS; sepsis; went disorder; kidney failure; cardiovascular disorder; cytostatic; angina pectoris; cerebral ischaemia; congenital heart defect; angina pectoris; cerebral ischaemia; congenital heart defect; angina pectoris; neurological disorder; Alzheimer's disease; parkinson's disease; inflammation; Crohn's disease; vulnerary; immunosuppressive, antibacterial; haemostatic; thrombolytic; antianginal; antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal; cerebroprotective; cardiant; nootropic; antiparkinsonian; antiinflammatory; gene; ss.
                                                                 GAAGTGCAGTTTGCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGG 1010
GlulleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
                                            GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly 320
                                                                                                                                                                                                                              cDNA sequence #164 containing coding region of a human secreted protein.
              891 GAAATCCTGCAGTCCAAGGTGCTTCCCTCCAAGGAAGAGCCAGTGAACACACAGTTATTCC
                                                                                        ACD82804 standard; cDNA; 3173 BP
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97US-0040162P.
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17-MAR-2000; 2000US-0190068P
                                                  YOUNG P E. GRERBE J M. FERRIE A M. DUAN D R. J. FLORENCE K A. OLLSEN H S. FISCHER C L. EBNER R. BEREWER R. MOORE P A.
            RUBEN S M.
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The present invention relates to the isolation of nover numbal Becreted proteins and the polynucleotide sequences encoding them. The invention also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins are useful for preventing, treating, sequences for the secreted proteins are useful for preventing, treating, ambliorating or diagnosing medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive disorders (e.g. leukaemia or breast cancers), wounds, reproductive thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or thrombocytopaenia), autoimmune disorders (e.g. Wiskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. Wiskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. AlbS or sepsis), renal control or fungal infections (e.g. AlbS or sepsis), renal disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina pectoris, cerebral ischaemia or congenital heart defects), respiratory disorders (e.g. Achaemiae), and inflammations (e.g. Crohn's disease). The polymucleotide or polypeptide may also be used as vaccine adjuvants.

ACD82641-ACD82950 encode human secreted proteins or their fragments. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral present invention relates to the isolation of novel human secreted Ferrie AM; Kyaw H; Ebner R; Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP; Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebne Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html Claim 4; SEQ ID NO 174; 260pp; English

Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

3173 328 0 0

Length: Matches: Conservative: Mismatches:

2.27e-163 1695.00 100.00% 100.00%

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Alignment Scores:

	Query DB:	/ Match:	99. 99.	Indels: Gaps:	00	
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	ą	171		CAAGTTAAAATCATTGC		
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	ò	141	LeuMetA	laSerValAsnSerThrCysAsnValThrLeuThrCysSer'	ValGluLysGlu	
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	ò	201		AlaArgGlnLeuCysAl	AsnasnSeraspSerIleSeralaArgGlnLeuCysalaAspIlealaMetGlyPheArg 220	
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22-AUG-1997;
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(SHIY/)
(LAFL/)
   cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.
                                                                                                                cDNA encoding novel human secreted protein seg id 174
                            ADI22889 standard; cDNA; 3173 BP.
                                                                                                                                                                                                                                                                                     97US-0038621P

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                                                                                    22-APR-2004 (first entry)
                                                                                                                                                                                                   US2003175858-A1
                                                                                                                                                                                                                                                                                                                                                                         07-MAR-1997;
11-APR-1997;
                                                                                                                                                                         Homo sapiens.
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                                                         ADI22889;
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                                    GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGGTAATGTCCTTCAAATC
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GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIle
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                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding a polynpeptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or amelicament for diagnosing, preventing, treating or amelicating a medical protein of the invention.
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                                                                                                                Ferrie AM;
                                                                                                                                                                                                                                                        New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition
                                                                                          Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AN
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;
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Best Local Similarity:
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          (ZENG/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
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ValAsnileGlnGluProArgGlnValLySileIleAlaTrpThrSerLySThrSerVal

1 MetalaGlnHisHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla 20

US-09-882-171-483 (1-329) x ADH73891 (1-3173)

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Length:
Matches:
Conservative:
Mismatches:
Indels:

2.27e-163 1695.00 100.00% 100.00% 99.94%

Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

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Gaps:

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GTAAATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTT
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New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

Claim 2; Fig 108; 695pp; English

Ϊ, Wood

Schoenfeld JR,

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Fong

χ,

Dennis

Clark H,

Chiu H, Wu ID,

(GETH) GENENTECH

WPI; 2004-329389/30.

P-PSDB; ADL82907

L5-SEP-2003; 2003WO-US029097 16-SEP-2002; 2002US-0411392P

WO2004024097-A2

25-MAR-2004.

Homo sapiens

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The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA transient hypogammaglobulinemia of infancy, Burkitt's IgA transient hypogammaglobulinemia of infancy, Burkitt's IgA propersonal intermediate Iyanhoma, follicular lymphoma, type II chremediate Iyanhoma, follicular lymphoma, type II chremediate Iyanhoma, follicular lymphoma, intermediate Iyanhoma, follicular lymphoma, con intermediate Iyanhoma, selective is the Iga or ankylosing spondylitis. The PRO proteins are also useful for propering a condition that is responsive to the PRO protein, e.g. cancer or immune mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
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Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic; Antiallergid; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer; immune-mediated inflammatory disease; human; gene; ss.

Human PRO24934 cDNA, SEQ ID 108

(first entry)

17-JUN-2004

Wood WI;

PM,

Williams

Van Lookeren M,

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Schoenfeld J,
(GETH ) GENENTECH INC
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                                                               LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
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           ThriyaArgTyrAsnLeuGlnileTyrArgArgLeuGlyLysProLysIleThrGlnSer
                                         GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle
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The invention relates to a novel isolated nucleic and and the FRO polypeptide encoded by it. A protein of the invention has antidiabetic, dermatological, antipsoriatic, antiallergic, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polymuclectide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the companied is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, cystemic sclerosis, and idopathic inflammatory myopathy, Sigren's systemic sclerosis, and idopathic inflammatory myopathy, Sigren's systemic sclerosis, and idopathic inflammatory myopathy, Sigren's systemic sclerosis, and disease, a demyelinating disease of the central or peripheral nervous cystem, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, corrents or autoimmune chronic active hepatitis, primary disease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Mulple's clisease, an autoimmune or immune-mediated skin disease, a bullous skin disease, asthma, allergic rhinitis, atopic dermatitis, psoriasis, an allergic chisease, asthma, allergic rhinitis, atopic dermatitis, food the costnophilis pneumonia, idopathic polymonary fibrosis, hypersensitivity or costnophilis pneumonia, interpreted sease, asthmassitivity, an immunologic disease of the lung, contained the processe, processed to the presensitivity of preumonitis, an immunologic disease of the lung, costnophilis pneumonia, indopathic pneumonia, remained the present sentined encodes a PRO protein of preumonia, processed the processes of parts of the present sentined the present sentined and processes of the preumonia processes and processes and processes 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               graft-versus-host disease. The present sequence encodes a PRO protein of the invention.
New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
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                                                                                                                                                                                             Claim 1; SEQ ID NO 1120; 2940pp; English
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Diagnosing susceptibility to schizophrenia (SC2) in a patient, by determining presence or absence of an allele of a linked polymorphic marker present on chromosome 1q22, were the marker is linked to a variant
                                                                                                                                                                                                                                  This sequence was isolated using the method of the invention as the SCZ gene. This sequence has been previously identified as CD84, GenBank Accession No. NM 008874. CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. The proteins encoded by this sequence may be involved in the processes by which the brain responds to biological stimuli. Therefore they may provide targets for therapeutic intervention in the treatment of schizophrenia. The SCZ sequence may be used in a new method comprises determining the presence or absence of an patient. The method comprises determining the presence or absence of an allele of a linked polymorphic marker in the DNA of the patient. The polymorphic marker is present in chromosome 1422 and is linked to a gene (SCZ) having a variant form associated with a phenotype of schizophrenia
                                                                                                                                                                                                                 Claim 19; Page 68-70; 82pp; English.
                                                            (RUTF ) UNIV RUTGERS STATE NEW
            23-APR-2001; 2001WO-US013040.
                                    21-APR-2000; 2000US-0198873P.
                                                                                     Brzustowicz LM, Bassett AS
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P-PSDB; AAB47878.
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TyrTyrGluArgileHisAlaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArg 100 120 140 464 164 344 404 Arescricascacciaresarcriscricririscriscracaaaccrescesaascascr 224 284 40 9 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn ThrLysArgTyrAsnLeuGln1leTyrArgArgLeuGlyLysProLys1leThrGlnSer MetAlaGlnHisHisLeuTrplleLeuLeuCeuCysLeuGlnThrTrpProGluAlaAla GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro ValAsnileGlnGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerVal Sequence 3300 BP; 957 A; 802 C; 750 G; 791 T; 0 U; 0 Other; 3300 328 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-882-171-483 (1-329) x AAI72383 (1-3300) 2.4e-163 1695.00 100.00% 100.00% 99.94% Percent Similarity: Best Local Similarity: Alignment Scores: н 45 105 41 165 61 225 101 345 121 405 21 81 285 g 셤 ò 요 ò g ò à 용

141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160

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SCZ; gene; CD84; platelet; monocyte; circulating B cell; schizophrenia; allele; polymorphic marker; chromosome 1q22; ss.

(first entry)

02-MAY-2002

CD84 coding sequence

sapiens

HOMO

Key

Location/Qualifiers 45. .1031 /*tag= a /product= "SCZ"

WO200202054-A2

10-JAN-2002

2; SEQ ID NO 6219; 210pp; English.

Example

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                                   The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma the method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleocide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
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                                                                                                                               GTAAATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACTGTT
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human secreted proteins, and encode the proteins given in AAX12521 to human secreted proteins, and encode the proteins given in AAX12521 to AAX12668, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producins secreted human gane products. They can also be used to develop products for diagnosis and therapy. The proliferation/differentiation activity, veal proliferation/differentiation activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, hemotactic/ chemokinetic activity, hemostatic activity, antiinflammatory thrombolytic activity, receptor/ ligand activity, antiinflammatory activity, tumour inhibition activity or other activity antiinflammatory call be used in forensic, gene therapy and chromosome mapping promoter.
                                                                                                                                                                                                               MetGluAspAlaGlyAspTyriysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; antiinflammatory; tumour inhibition; antitumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from umbilical cord, lymph ganglia, lymphocytes and placental tissue.
                                                        AlaTyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                                             GCTTATGTAACAGTAGGAGAATAATAAACAGGAGNGGTAGTTACTGCCACCCCCCCC
                                                                                                                                    TyrtyrgluargileHisAlaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArg
                                                                                                                                                                          618 TATTATGAAAGGTTANATGCTTTAGGTTCGAACTACAATTTGGTCATTAANGATTTGAGG
                                                                                                                                                                                                                                       Human secreted protein 5' EST SEQ ID NO: 41 from WO 9906553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating, and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaGlnHisHisLeuTrplleLeuLeuCysLeuGlnThrTrpProGluAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 748 BP; 246 A; 164 C; 164 G; 171 T; 0 U; 3 Other;
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                                  1393 ACTTCAAGCTATGAAATTGTGATC 1416
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                ThrSerSerTyrGlulleValile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-020520P.
09-JUN-2000; 2000US-0211315P.
25-JUL-2000; 2000US-0220534P.
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41 ValAsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal

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                                                                                                                                      sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
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TITLE OP INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PC002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER PILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
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US-08-880-875-1

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US-08-348-792-3

US-08-139-955-3

US-09-188-545-258

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Patent No. 6420526
GENERAL INFORMATION:
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Sequence 1456, Ap
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Ygapop 10.0 , Ygapext
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RESULT 2
US-09-949-016-1456

1 Sequence 1456, Application US/09949016

2 Settent No. 681239

3 GENERAL INFORMATION:

1 TILLE OF INVENITON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

1 TILLE OF INVENITON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

2 TILLE OF INVENITON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

3 TILLE OF INVENITON: WIMBER: US/09/949,016

4 CURRENT APPLICATION NUMBER: 60/241,755

5 PRIOR APPLICATION NUMBER: 60/241,755

6 PRIOR PILING DATE: 2000-10-20

7 PRIOR PLING DATE: 2000-10-03

7 PRIOR FILING DATE: 2000-10-03

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                                                                                                                  SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr
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BARLIER APPLICATION NUMBER: 60/056,875
BEARLIER FILING DATE: 1997-08-22
BEARLIER FILING DATE: 1997-08-22
BEARLIER FILING DATE: 1997-08-22
BEARLIER FILING DATE: 1997-08-22
BEARLIER APPLICATION NUMBER: 60/056,887
BEARLIER FILING DATE: 1997-08-22
BEARLIER FILING DATE: 1997-08-22
BEARLIER FILING DATE: 1997-08-26
BEARLIER FILING DATE: 1997-06-06
BEARLIER FILING DATE: 1997-06-06
BEARLIER APPLICATION NUMBER: 60/056,884
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BEARLIER APPLICATION NUMBER: 60/056,884
BEARLIER FILING DATE: 1997-09-05
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BEARLIER APPLICATION NUMBER: 60/051,669
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Matches:
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaetSEQ for Windows Version
; SEQ ID NO 557
; LENGTH: 3299
; TYPE: DNA
; CRGANISM: Human
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Sequence 557, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERE

TILLE REFERENCE: CLO01307

CURRENT PILING DATE: 2000-04-14

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08
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                                            TyrTyrGluArg1leHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg
                                                                                         MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr
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                                                        LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
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Sequence 13198, Application US/09949016
; Sequence 13198, Application US/09949016
; Batent No. 681239
; GENERAL INFORMATION:
; TAPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WINBER: US/09/949,016
; CURRENT PELING DATE: 2000-04-14
; CURRENT PELING DATE: 2000-10-20
; PRIOR PELING DATE: 2000-10-20
; PRIOR PELING DATE: 2000-10-33
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 5000-109
; SEQ ID NO 13198
; LENGTH: 37492
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i Sequence 12299, Application US/09949016

j Patent No. 6812339

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF,

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF,

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-12299
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O'S-69-221-357-33

Pagenene 53, Application US/09227357

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Patter No. 6345281

Patter No. 6345281

PALLICANT: Fistone et al.

TILLE OF INTERNITYON: 123 Human Secreted Proteins FILE REPERINCE: P220101

PALLIER PELLICATION NUMBER: 05/09/27, 337

CURRENT PALLICATION NUMBER: 06/051, 266

BALLIER PELLICATION NUMBER: 06/051, 265

BALLIER PELLICATION NUMBER: 06/051, 265

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BALLIER PELLICATION NUMBER: 06/051, 263

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99 TGGCTGCTTCTTCTCCTGCTGCTGCTCCAGGARGCCAAAGGAAACTCTGGAAGATGGTGT 158
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204 CCCCTGGAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCACAAAGT
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EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER PELICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
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49.83%
31.83%
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US-09-227-357-53
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Best Local Similarity:
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JAPELCANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOTIANE: FESTSEQ for Windows Version 4.0

LENGTH: 2440
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Mismatches:
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APPLICAMT: VENTER, J. Craig et al.

APPLICAMT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN INSEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSELESE FOR WINDOWS Version 4.0

LEMENTH: 2440
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Patent No. 6812339
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US-09-0	US-09-882-171-483 (1-329) x US-09-949-016-1454 (1-2440)	DD 1140 ICIGGATCCAGGAAGAGAA
ò		
•	8 IleLeuLeuCysLeuGlnThrTrpProGluAlaAlaGlyLysAspSerGlu 25	RESULT 9 US-08-348-792-7
Dp	204 ATACTCCTCCTCCTCAGGGTGTATCAGGGCAAAGGATGCCAGGGATCAGCTGACCAT 263	; Sequence 7, Application US/08348 ; Patent No. 5576423
ò	26 IlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProValAsnIleGlnGlu 45	GENERAL INFORMATION: ; APPLICANT: Aversa, Gregorio
g G	- <u>8</u>	AFFLICANT: Chang, Chia-Chun APPLICANT: Cocks, Benjamin
ò	46TroArgGlnValLysllelleAlaTrpThrSerLysThr 58	AFFILEMNI: GE VIIES, JAH E. ITHIB OF INVENTION: PURIFIED ITHIR OF INVENTION: STREAM
qq	303 AACAGCATACAGACGAAGGTTGACAGCATTGCATGAAGAAGAAGTTGCTGCCCTCACAAAAT 362	NUMBER OF SEQUENCES: 12
ò	59 ServalAlaTyrvalThrProGlyAspSerGluThrAlaProvalValThrvalThrHis 78	CORRESPONDENCE ADDRESS: ADDRESSEE: DNAX Research I.
QQ	363 GGATTTCATCACATATTGAAGTGGGAGAATGGCTCTTTGCCTTCCAATACTTCCAAT 419	Palo
ò	79 ArgAsnTyrTyrGluArglleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAsp 98	; SIAIE: CAINIONNA ; COUNTRY: USA
qq	420GATAGATTCAGTTTTATAGTCAAGAACTTGAGTCTTCTCATCAAGGCA 467	COMPUTER READABLE FORM:
δ	99 LeuargMetGluAspalaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyr 118	; COMPUTER: IBM PC compatibl
qq	468 GCTCAGCAGCAGGACAGTGGCCTCTACTGCCTGGAGGTCACCAGTATATCTGGAAAA 524	; OPERATING SYSTEM: PC-DOS ; SOFTWARE: PatentIn Relea
ò	119 ThrThrThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr 138	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/0
QQ	525 GTTCAGACAGCCACGTTCCAGGTTTTTGTATTTGATAAAGTTGAGAAACCCCGCCTACAG 584	; FILING DATE: 02-DEC-1994 ; CLASSIFICATION: 530
δλ	139 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 158	; ATTORNEY/AGENT INFORMATION: ; NAME: Ching, Edwin P.
qq	585 GGGCAGGGAAGATCCTGGACAGAGGGAGATGCCAAGTGGCTCTGTCTTGCTTG	; REGISTRATION NUMBER: 34,09 ; REFERENCE/DOCKET NUMBER: D
ò	159 LysGluGluLysAsnThrTyrAsnTrpSerProLeuGlyGluGlu 174	U :::
QQ	645 AGGGATGGCAATGTGTTTGGTACAGAGGGAGCAAGCTGATCCAGACAGCA 701	; INFORMATION FOR SEQ ID NO: 7
ζ	PheGlnThrProGl	; SEQUENCE CHARACTERISTICS: ; LENGTH: 1079 base pairs
QQ	702 GGGAACCTCACCTACCTGGACGAGGAGGTTGACATTAATGGCACT 746	; TYPE: nucleic acid ; STRANDEDNESS: single
ò	190ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAla 208	OGY: line E TYPE: c
qq	747 CACACATATACCTGCAATGTCAGCAATCCTGTTAGCTGGGAAAGCCACACCTGAATCTC 806	CDS
δ	209 ArgGlnLeuCysAlaAspIleAlaMetGlyPheArgThrHisHisThrGlyLeuLeuSer 228	. LOCATION: 1531073 US-08-348-792-7
đ	807 ACTCAGGACTGTCAGAATGCCCATCAGGAATTCAGA	nment Scores:
ò	229 ValLeuAlaMetPhePheLeuLeuValLeuIleLeuSerSerValPheLeuPheArgLeu 248	Score: 195.50
qq	843TITIGGCCGITITIGGTGATCATCGTGATTCTAAGCGCACTGTTCCTTGGCACCCTT 899	larity: imilarity:
ò	249 Phe	. Query Match: 11.53% DB: 1
qq	900 GCCTGCTTCTGTGTGGAGGAGAAGGAAGAAGCAGTCAGAGACAGAC	US-09-882-171-483 (1-329) x US-08
ογ	260ThrileTyrThrTyrIleMetAlaSerArgAsnThrGlnProAla 274	Oy 12 CysieuGlnThrTrpProGlu
qq	960 GAATTITGACAATTIACGAAGATGTCAAGGATCTGAAAACCAGGAGAATCACGAGCAG 1019	Db 129 TGCCTGTGAGTGG
λ	275 GluSerArglleTyrAspGlulleLeuGlnSerLysVal 287	Qy 32 IleLeuGlyGluSerValThr
Ob	1020 GAGCAGACTTTTCCTGGAGGGGGGGACCATCTATGATCCAGTCCCAGTCTTCT 1079	Db 180 CAGTIGGGAAGCAAAGIGCTG
ò	288 LeuproSerLysGluGluproValAsnThrValTyrSerGluValGlnPheAlaAspLys 307	Qy 47 ArgGlnValLysIlelleAla
đ	1080 GCTCCCACGTCACAGAACCTGCATATACATTATATTCATTAATTCAGCTTCCAGGAAG 1139	740 AAAAGCATCACATGATGATGATGATGATGATGATGATGATGATGATGATGA

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laTrpThrSerLysThr-----5er 59
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TCACAATGGCAAATCACTGGAGAACAGTGTCGAGAACAAA 299
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                   415-496-1200
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STRANDEDNESS: single
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                           Palo Alto
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Best Local Similarity:
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US-08-462-738-7
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                                                                                                                                                                           120 ThrThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIle 137
                        ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
                                                                                                                                                                                                                                     ThrGlnSerLeuMetAlaSerValAgnSerThrCygAsnValThrLeuThrCygSerVal 157
                                                                                     360 TTTTATCTGGAG-------AATCTCACCCTGGGGATACGGAAAGC 398
                                                        80 AsnīyrTyrGluArglleHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeu 99
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                                                                                                                                                                                                                                                      GlutysGluGlutysAsnValThrTyrAsnTrpSer---------Probeu
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                                                                                                                                               399 AGGAAGGACGATGAGGGATGGTACCTTATGACCCTG------GAGAAAATGTT
                                                                                                                                                                                                        447 TCAGTTCAGCGCTTTTGCCTGCAGTTGAGGCTTTATGAGCAGGTCTCCACTCCAGAAATT
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GinLeuCysAlaAspileAlaMetGlyPheArgThrHis------
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56
124
81
                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SEGIFFARION DATA:

APPLICATION NUMBER: US/08/462,738

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/348,792

FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: CALIGG, Edwin P.

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: 34,090
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
901 California Avenue
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PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELEPHONE: 415-852-9196
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                         -----GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeu 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                             241 SerSerValPheLeuPheArgLeuPheLysArgArg----------GlnAsp 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               843 CAG---------TTGAGAAGAAGAAGAAGAACGAACCAATTACCAGACA 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 AlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg------- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AsnThrGlnProAlaGlu-----SerArglleTyrAspGlulleLeu 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          942 AAGAAACTTGACTTCCCAGCTCGAGGACCCTTGCACCATGTAT-----GTTGCT 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 GlnSerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGlu 301
                                                            AAAGTTTTAAACAAGACCCAGGAGAAACGGGACCTGCACCCTTGATACTGGGCTGCACAGTG
                                ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal
                                                                                                       -----ProLeu
                                                                                                                                                                                          190 ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArg
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882 ACAGTGGAAAAAAAAGGCTTACGATCTATGCCCAAGTCCAGAAACCAGGTCCTCTTCAG
                                                                                                                                                                                                                                                                                                          210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis--------
                                                                                                                                                                                                                                                                                                                                                                            -----HisThrGlyLeuLeuSerValLeuAlaMetPheLeuLeuValLeuIleLeu
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Patent No. 6372899

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Chia-chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de vites, Jan B.
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
INVERS OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                    GluLysGluGluLysAsnValThrTyrAsnTrpSer-----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
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300 ATAGTGTCTCTTGATCCATCCGAAGCAGGCCCTCCACGTTATCTAGGAGATCGCTACAAG 359
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                                                                                                                                                                                                                                                                                                                                                                                                           100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLyglle 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeu 189
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                                                                                                                                                                                                                                                                                          32 IleLeuGlyGluSerValThrPhePro------ValAsnIleGlnGluPro 46
                                                                                                                                                                                                                                                                                                                      180 CAGTIGGGAAGCAAAĞIGCIGCIGCIGCCCIGACAIATĞAAAGGAIAAAIAAGAGCAIGAAC
                                                                                                                                                                                                                                                                                                                                                                            47 ArgGlnValLysIleIleAlaTrpThrSerLysThr--------Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 AAAGTITIAAACAAGACCCAGGAAACGGGACCTGCACCTTGATACTGGCCTGCACAGTG
                                                                                                                                                                                                     CysLeuGlnThrTrpProGluAlaAlaGlyLysAspSerGluIlePheThrValAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg
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1079
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124
81
Length:
Matches:
Conservative:
Mismatches:
Indels:
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47 ArgGlnValLysileIleAlaTrpThrSerLysThr------
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                  Gaps:
          INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1079 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                        3.02e-14
195.50
39.88%
23.46%
415-496-1200
                                                                                                                                  CDS
153..1073
                                                                                                MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-880-875-7
                                                                                                                                                                                              Alignment Scores:
 TELEFAX:
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                                                                                                                                                                                                                                          843 CAG-------TTGAGAAGAGGAGGTAAAACGAACCATTACCAGACA 881
 624 AACCCAGCCAACAGCTCCCACCTCCTGTCCCTCACCCTCGGCCCCCAGCATGCTGACAAT 683
                               190 ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArg 209
                                                -------AGGACAGACCCTCAGAACAAAACCATGG
                                                                                                                                                                  241 SerSerValPheLeuPheArgLeuPheLysArgArg--------GlnAsp
                                                                                                                                                                                                                                                                                       942 AAGAAACTTGACTTCCTTCCAGGTCCTTGCACCATATAT-----GTTGCT
                                                                                      210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis------
                                                                                                                                                   -----HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu :::::|||||||||
                                                                                                                                                                                                                                                                      255 AlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: We of Vies, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
PILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436K
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/0880875
Patent No. 6199065
GENERAL INFORMATION:
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ADDRESSEE: DNAX Rese
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-880-875-7
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744 CCCGGATGC------AGGACAGACCCCTCAGAAACAAAACCATGG 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluLysGluGluLysAsnValThrTyrAsnTrpSer-------ProLeu 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 TITTATCTGGAG-------AATCTCACCCTGGGGATACGGGAAAGC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal 157
                                                         129 TGCCTGTGTGAGTGG-----GGTGGGCGCATGATGAACTGCCCAAAGATTCTCCGG 179
                                                                                                                                                                                                                                                                              300 ATAGIGICITITGAICCAICCGAAGCAGGCCCICCACGIIAICIAGGAGAICGCIACAAG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 AGGAAGGAGGATGAGGATGGTACCTTATGACCCTG------GAGAAAAAATGTT 446
                                                                                                                                                                                                                                                                                                                                                          60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 AsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
                                                                                                                         --- ValAsnIleGlnGluPro 46
CysieuGlnThrTrpProGluAlaAlaGlyLysAspSerGluIlePheThrValAsnGly 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   624 AACCCAGCCAACAGCTCCCACCTCCTCACCCTCGGCCCCCAGCATGCTGACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis------
                                                                                                                                                                                   180 CAGTIGGGAAGCAAAGIGCIGCIGCIGCCTGACAIAIGAAAGGAIAAAIAAGAGCAIGAAC
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566

623

Best Local Similarity: 23.75% Mismatches: 112 Query Match: 11.44% Indels: 78 DB: 1 Gaps: 16 . US-09-882-171-483 (1-329) x US-08-348-792-1 (1-1716)	Qy 33 LeuGlyGluSerValThrPheProValAenIleGlnGluProArg 47	48 GlnValLys1le11eAlaTrpThrSerLysThrSerVal :::	AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn ::: ::::: GTGTCTCTTAGATCCGAAGCAGGCCCTCCACGTTATCTAGGAGAAGTAGTAGTTAGATACTAGAAGTAGTAGTTT		101 MetGluAspAlaGlyAspTyrLysAlaA	Qy 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr 138	Oy 139 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 158	Qy 159 LysGluGluLysAsnValThrTyrAsnTrpSer	Oy 172GlygluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 190	Oy 191 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArgGln 210		Qy 223HisThrGlyLeuLeuSerValLeuAlaMetPheDeLeuValLeuIleLeuSer 241 :::	Qy 242 SerValPheLeuPheArgLeuPheLysArgArg	Oy 256 AlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg259	Oy 270AsnThrGlnProAlaGluSerArgIleTyrAspGluIleLeuGln 284	Oy 285 SerLysValLeuProSerLysGluGluProValAsnThrValTyrSerGluVal 302	RESULT 14 US-08-462-738-1 ; Sequence 1, Application US/08462738
Db 783 GCAGTGTATGCTGGGCTGTTAGGGGGTGTCATGATGTTCTCATCATGGTGGTAATACTA 842 Qy 241 SerSerValPheLeuPheArgLeuPhelysArgArgGlnAsp 254 Db 843 CAGTTGAGAAAGAAAGAAGAAACGAACCATTACCAGACA 881	Qy 255 AlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg 269	Qy 270AbnThrGlnProAlaGluSerArglleTyrAspGluIleLeu 283	Qy 284 GlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSerGlu 301 Db 996 GCCACAGAGCCTGTCCAGAGACTCTGTCCAGAAATTCCATCACAGTCTATGCTAGT 1055	Qy 302 Val 302 Db 1056 GTG 1058	RESULT 13 US-08-348-792-1 ; Sequence 1, Application US/08348792 ; Patent No. 5576423	; GENERAL INFORMATION: ; APPLICANT: Aversa, Gregorio ; APPLICANT: Chang, Chia-Chun J. ; APPLICANT: Cocks. Benjamin G.	de Vri NVENTION NVENTION SEQUENCES	CORRESPONDENCE ADDRESS: ADDRESSEE: DNAX Research Institute STREET: 901 California Avenue CITY: Palo Alto	STATE: California COUNTRY: USA I ZIP: 94304-1104 COMPUTER READARIE FORM.	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible DOPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: PatentTn Paleace #1 0 Varcion #1 05	LICATION DATA: DN NUMBER: US/08/348,792 TE: 02-DEC-1994	8 A E	96 1:	; SEQUENCE CHARACTERISTICS: ; LENGTH: 1716 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: sincle	ine	10N: 12-1	Pred. No.: 9.83e-14 Length: 1716 Score: 194.00 Matches: 76 Percent Similarity: 40.62% Conservative: 54

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937 AAACTIGACTCCCTCCCAGCTCAGACCCTTGCACCACATAT-----GTTGCTGCC 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 SerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGluVal 302
                                                                                                                                                                                                                                                                         242 SerValPheLeuPheArgLeuPheLysArgArg-------GlnAspAla 255
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877 GTGGAAAAAAAAAGCCTTACGATCTATGCCCAAGTCCAGAAACCAGGTCCTCTTCAGAAG 936
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                                                                              121 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 138
                                                                                                                                                                                                                                                 LysGluGluLysAsnValThrTyrAsnTrpSer--------ProLeu--- 171
                                                                                                                                                                                                                                                                                                                                                               619 CCAGCCAACAGCTCCCACCTCTGACCTCGGCCCCCAGCATGCTGACAATATC 678
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                                                                                                         ---GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 190
                                                                                                                                                                                                                                                                                                                                                                                                                     TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArgGln 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 ---HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeuSer 241
101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
                                                                                                                                                                139 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 LeuCysAlaAspIleAlaMetGlyPheArgThrHis-------
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| Sequence 1, Application US/09199955
| Sequence 1, Application US/09199955
| Patent No. 6372899
| GENERAL INFORMATION:
| APPLICANT: Aversa, Gregorio | APPLICANT: Chang, Chia-Chun J. APPLICANT: Chang, Chia-Chun J. APPLICANT: Chang, Chia-Chun J. APPLICANT: Cocks, Benjam G. APPLICANT: Cocks, Benjam G. APPLICANT: Gover, Benjam G. TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES | UNMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSE: DARK Research Institute | STREET: 901 California Avenue | CITY: Palo Alto | STATE: California COUNTRY: USA | 27P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg----
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ZIP: 94304-1104

WOODTURR READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PALENTER PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                       394 AAGGAGGATGAGGATGGTACCTTATGACCCTG-
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APPLICANT: Chang, Chia-Chun J. APPLICANT: Chang, Chia-Chun J. APPLICANT: Cocks, Benjamin G. APPLICANT: de Vries, Jan B. TITLE OF INVENTION: FURIFIED GENES ENCODING MAMMALIAN CELL TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Records
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnValLysIleIleAlaTrpThrSerLysThr------
                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-882-171-483 (1-329) x US-08-462-738-1 (1-1716)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0436GB
TELECOMMUNICATION NUMBER: DX0436GB
TELECOMMUNICATION NUMBER: DX0436GB
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TELECOMMUNICATION NUMBER: DX0436GB
TELECOMMUNICATION NUMBER: DX0436GB
TELEPHONE: 415-496-120
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901 California Avenue
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40.62%
23.75%
11.44%
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: California
COUNTRY: USA
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Best Local Similarity:
Query Match:
DB:
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LOCATION:
US-08-462-738-1
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                               FILING DATE: 05-UN-1955
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P. REGISTAATION NUMBER: 34,090
REPERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
FELEPHONE: 415-496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERICICS:
LENGTH: 1716 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
APPLICATION NUMBER: US/09/199,955
                                                                                                                                  US 08/461,473
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194.00
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23.75%
                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
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; LOCATION: 61..1065
US-09-199-955-1
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MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity:
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DB:
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191 TyrThrCygThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArgGln 210 	211 LeuCysAlaAspIleAlaMetGlyPheArgThrHis	223HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeuSer 241 	242 SerValPheLeuPheArgLeuPheLysArgArg	256 AlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg	270AsnThrGlnProAlaGluSerArglleTyrAspGluIleLeuGln 284 ::::: ::: 937 AAACTIGACTCCTAGCACCCTTGCACCACCATATATGTTGCTGCC 990	SerLysValLeuProSerLysGluGluProValAsnThrValTyrSerGluVal 302
19	21 73	223	242	256	270	285
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Search completed: February 5, 2005, 11:31:47 Job time : 239.449 secs

Sequence 174, Seguence 174, Seguence 6219

Sequence Sequence Sequence 1

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Sequence 1 Sequence 1

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Sequence 29, Application US/10436523

Sequence 29, Application US/10436523

Publication No. US20030180888A1

GENERAL INFORMATION:

APPLICANT: Fraser, Christopher C.

TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

FILE REFERENCE: 7853-244-999

CURRENT APPLICATION NUMBER: US/10/436,523

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 2001-11-20

PRIOR FILING DATE: 2000-11-03

NUMBER OF SEQ ID NOS: 100

SOFTWARE: PARENTING PARE: 2000-11-03

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-DS=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL10 -LOOPEXT=0 -UNITS=bits -STRAT=1 -BND=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=50 -THR SCORE=pct -THR MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=50 -THR SCORE=pct -THR MAX=100
-MAXIEN=200000000 -USER=LSO9882171 @CGN 1 1 582 @runat 04022005 114005_26092
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-245-770-75

ALIGNMENTS

Sequence Sequence

SUMMARIES

TYPE: DNA ORGANISM: Homo sapiens

us-09-882-171-483.rnpb

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RESULT 2
US-10-723-860-1885

US-10-723-860-1885

Squence 1885, Application US/10723860

Publication No. US20040253606A1

GENERAL INPORMATION:
APPLICANT: Alazaha

APPLICANT: Clotnik, Albert

TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

FILE REFERENCE: 05882.0193.NPUS01

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NOS: 8393

SEQ ID NOS: 8393

SEQ ID NOS: 8393
   161 GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
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; Sequence 174, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT ETLING DATE: 2001-03-16
; Prior application data removed - consult PALM or fi
; NOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 174
: LENGTH: 3173
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                                                              291 TATTATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGG
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Publication No. US20030175858A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
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FILE REPERRUCE: PZ002PZ
CURRENT APPLICATION WORRER: US/09/082,171
CURRENT APPLICATION WORRER: 108/09/391
PALOR FILING DATE: 2001-05-18
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PALOR FILING DATE: 2001-05-18
PALOR FILING DATE: 1996-05-08
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PRIOR APPLICATION NUMBER: 60/043,569
PRIOR PILING DATE: 1997-04-11
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                                                                                                                                                                                                                                                                                      Sequence 174, Application US/10164861
Fublication No. US20030225248A1
GENERAL INFORMATION:
APPLICANT: BERENCE: E200291
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT PILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PATENTING UNIMBER: ECT/US98/04493
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Sequence 6219, Application US/10723860
; Bedulcation No. US20040253606A1
; Beblication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Alazi, Matsaha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Compositions &; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, CURRENT FILING DATE: 2003-11-26
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SEQ ID NOS: 8393
; SEQ ID NO SEQ 1300
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                                  AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
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ORGANISM: Homo sapiens
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Best Local Similarity:
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TYPE: DNA
PREATURE:
NAME/KEY: SITE
LOCATION: (3119)
OTHER INFORMATION: n equ
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NAME/KEY: SITE
LOCATION: (3121)
OTHER INFORMATION: n equ
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Best Local Similarity:
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PREVENTION,
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US-10-198-846-13255

Sequence 13255, Application US/10198846

PUDLICation No. US2003009974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Wangy Youzhen
APPLICANT: Wangy Youzhen
TITLE OF INVENTION: NOVEL GENES
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, FILE REFERENCE: MRI-049
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084

SEQ ID NO 13255

LENGTH: 3687
                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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         3676,
3686,
         3673, 3674, 3675,
3683, 3684, 3685,
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                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3669, 3670, 3671, 3672,
; LOCATION: 3678, 3679, 3680, 3681, 3682,
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13255
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                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr---GlnSer 140
                     -----GTAACCATTATGGTCAAAAGCTAC 320
                                                                                    CTGGGCCGACTAGACATCACCAAGTGGAGTTACTCCCTGTGCATCAGCAATCTGACTCTG 380
                                                                                                                                         GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 121
                                                                                                                                                                                 381 AATGATGCAGGATCCTACAAAGCCCAGATAAACCAAAGGAATTTTGAAGTCACCACTGAG 440
                                                                                                                                                                                                                                                411 GAGGAATTCACCCTGTTCGTCTATGAGCAGCTGCAGGAGCCCCAAGTCACCATGAAGTCT 500
                                                                                                                                                                                                                                                                                                           LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
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GAGAAAAGTGTTCTGTACAGCTGGACCCCAAGGAACCCCATGCTTCTGAGTCCAATGGA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCysThr 194
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APPLICANT: WAKELAND, WARD
APPLICANT: WAKELAND, MAY
APPLICANT: WANNSTRADT, ANY
APPLICANT: WORKELAND
TITLE OF INVENTION: ISOLATION OF GENES WITHIN SLE-1B THAT MEDIATE A BREAK
TITLE OF INVENTION: ISOLATION OF GENES WITHIN SLE-1B THAT MEDIATE A BREAK
TITLE OF INVENTION: ISOLATION OF GENES WITHIN SLE-1B THAT MEDIATE A BREAK
CURRENT PELICATION NUMBER: 0/09/660,836B
CURRENT FILING DATE: 2002-08-13
PRIOR PHILING DATE: 2002-08-13
SPRIOR PLILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PRECEIT VET: 2.1
                                                               82 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .......AAATCCAGGATCCTTACAAGAACAGGGTGTGG 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 TyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyr 279
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          TTCGCACGTCCCAAAGAAAT-
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ORGANISM: Homo
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LENGTH: 2286
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                                                               GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly.320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 81
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                                                                                                                                                                                                                                                                                                                      GAPPLICANT: YUE, Henry; XU, Yuming;
APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget M.;
APPLICANT: TRNG, Y: Tom; DUGGAN, Brendan M.;
APPLICANT: TRAN, Uyen K.; BAUGHN, Mariah R.;
APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
APPLICANT: MASON, Patricia M.;
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-025 SUN;
FILE REPRENCE: PC-025 SUN;
CURRENT APPLICATION NUMBER: US-010, A71, 449
CURRENT FILING DATE: 2003-09-10
PRIOR PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275, 249
PRIOR APPLICATION NUMBER: US 60/216, 810
PRIOR APPLICATION NUMBER: US 60/316, 810
PRIOR APPLICATION NUMBER: US 60/316, 810
PRIOR APPLICATION NUMBER: US 60/32, 977
PRIOR APPLICATION NUMBER: US 60/348, 447
PRIOR APPLICATION NUMBER: US 60/348, 447
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PERL PROGRAM
SEQ ID NO 20
LENGTH: 1849
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OTHER INFORMATION: Incyte ID No: 7500099CB1
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                                                                                                                                                                                     1393 ACTICAAGCTATGAAATTGTGATC 1416
                                                                                                                                               ThrSerSerTyrGluIleValile 328
                                                                                                                                                                                                                                                                 Sequence 20, Application US/10471449 Publication No. US20040097711A1 GENERAL INFORMATION:
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Best Local Similarity:
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LyshsnyalThrTyrAsnTrpSerProLeu-------GlyGluGluGly 175
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                                                                                                                                                                                                                                                                                                                    TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
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ATCTCAGTAGACACAGAGATTGAGAACGTCATCTGGATTGGTCCCAAAAATGCTCTTGCT
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                                                                                                                                                                                                                                                                                                        GlnHisHisLeuTrplleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAlaGlyLys
 TITLE OF INVENTION: Methods of therapy and diagnosis using targeting TITLE OF INVENTION: that express Ly-9 FILE REFERENCE: HYS-68 CURRENT APPLICATION NUMBER: US/10/310,612 CURRENT FILING DATE: 2002-12-04 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin version 3.1
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98
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Mismatches:
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                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asp-----IlealaMetGlyPheArgThrHisHisThrGlyLeuLeuSerValLeuAla 231
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TIGTTTAACACATCCATCATTAGCAAAGAGAGAAGAAGCAGCAGCAACGGCAGATCCACTC
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atctcagtagacacagagattgagaagtcatctggattggtcccaaaaatgctcttgct
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                                                                                                                                                                                                                                                                                                                                                                                                                                   43 IleGlnGluProArgGlnValLysllelleAlaTrpThrSer---LysThrSerValAla
                                                                                                 GlnHisHisLeuTrp1leLeuLeuCysLeuGlnThrTrpProGluAlaAlaGlyLys
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         Conservative:
Mismatches:
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US-10-510-612-1
, Sequence 1, Application US/10310612
, Publication No. US20040109862A1
, GENERAL INFORMATION:
         54.03%
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Percent Similarity:
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Query Match:
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---ValPheLeu

760 CCAGGAGCTCCCAGAGGAACAACGGGGGAGACT---GTGGTAGGGGTCCTGGGAGA

g

APPLICANT: Emtage, Peter

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215 -----IleAlaMetGlyPheArgThrHisHisThrGlyLeuLeuSerValLeuAlaMet 232
                                                                                                                                                                           233 PhePheLeuLeuValLeuIleLeuSerSer-------ValPheLeu 245
                                                                                                                                                                                                                          817 CCAGTCACCCTGCCACTTGCCACTCCCGGGACACAGAGAAGGTTGTCTGGTTG 876
                                                                                                                                                                                                                                                             PheArg------LeuPheLygArgGlnAspAlaAlaSerLysLysThrlleTyr 262
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                640 recarretracegrerecegacacarereaceceagacerecearacarereceaece
                                                                                                      196 GlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCysAlaAsp
                                                                                                                          GlyGluGluGly
                                                      176 AsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAla
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Mismatches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                                                                                 Sequence 1, Application US/10328538
Publication No. US20040109863A1
GENERAL INFORMATION:
APPLICANT: Emtage, Peter
TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of cells
TITLE OF INVENTION: that express Ly-9
FILE REPERENCE: HYS-68CP
CURRENT APPLICATION NUMBER: US/10/328,538
CURRENT FILING DATE: 2002-12-04
PRIOR PILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                        PheArg------LeuPheLysArgArgGlnAspAlaAlaSerLysLysThrIleTyr 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400 AATGATCCAGATCCTACAAAGCCCAGATAAACCAAAGGAATTTTGAAGTCACCACTGAG 459
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317 CCAGTCACCTGCCACTTGCACTCCCAGCCTGCCGGGACACACAGAAGGTTGTCTGGTTG
                                         43 IleGlnGluProArgGlnValLysllelleAlaTrpThrSer---LysThrSerValAla
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Mismatches:
Indels:
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Matches:
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52.86%
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Best Local Similarity:
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AlaAspIleAlaMetGlyPheArgThrHisHisHisThrGly------LeuLeuSerVal 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrAlaGlnAsnProValSerAsn---AsnSerAspSerIleSerAlaArgGlnLeuCys 212
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                                                                       US-09-882-171-483 (1-329) x US-10-436-523-74 (1-1139
 Mismatches:
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241 CACTACCAGGGCCAAGTGAGCTTCCTGGACCCCAGCTATTCCCTGCAATCTG 300
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   100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr
                                                                                                                                                      301 AGCTGGGATTCAGGGCTTTACCAAGTCAAGTCAACCTGAGAACATCCCAGATCTT
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                                                            80 AsnTyrTyrGluArg1leHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeu
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TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
TITLE REPRENCE: 7853-244-992
CURRENT APPLICATION NUMBER: US/10/436,523
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: US/10/007,303
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-30
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US-10-436-523-74
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SEQ ID NO 74
LENGTH: 1139
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APPLICANT: No. US20030124575Alartis AG
APPLICANT: No. US20030124575Alartis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: No. US20030124575Alartis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: Phares, William
APPLICANT: Jaritz, Markus
APPLICANT: Jaritz, Markus
APPLICANT: Lapp, Hilmar
APPLICANT: Kalthoff, Frank Stephan
ITILE OF INVENTION: Organic Compounds
FILE REFREENCE: 4-31347 PCT
CURRENT APPLICATION NUMBER: US 60/120, 946
CURRENT PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 60/205, 026 (US 60/279, 243)
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-19
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PRIOR PLING DATE: 2000-05-19
PRIOR PLING DATE: 2000-05-19
PRIOR PLING DATE: 2000-05-19
ThralaGlnAsnProValSerAsn---AsnSerAspSerIleSerAlaArgGlnLeuCys 212
                                                                     AlaAspIleAlaMetGlyPheArgThrHisHisThrGly------LeuLeuSerVal 229
                                                                                                          745 GCAGATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCCTTCTGCCTCCTGGCCAAGGGA 804
                                                                                                                                                 LeuAlaMetPhePheLeuLeuValLeuIleLeuSerSerValPheLeuPheArgLeuPhe 249
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SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: n = A,T,C
US-10-220-946-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 TGGCTGCTTCTTCTCCTGCTGCTCCAGGAGGCAGCCAAAGGAGGACTCTGGAATGGTGT 159
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                   APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: $32682000100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIOR FILING DATE: 2002-06-18
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2001-12-10
NUMBER: OF SEQ ID NOS: $49
SEQ ID NO 132
LENGTH: 1139
                                    Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
   Robert Alan
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50.87%
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; ORGANISM: Homo Sapiens
US-10-170-385-132
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Query Match:
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213 AlaAspileAlaMetGlyPheArgThrHisHisThrGly------LeuLeuSerVal 229
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                                                                            205 CCCCTGGAAATACCACCAGATGAAGAGTTGAGAACATCATCTGGTCCTCTCACAAAGT 264
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-----GTGGTTGCGTCCTTCAGGAGTCCATCAGCCTC 204
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BY207872 EST64278 Pan trogl

Mus muscu BY199370

Homo sapi BP300475

AL561509 AL561522

Sequence:

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1 (bases 1 to 987)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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VIRTUAL TRANSCRIPT, partial sequence,
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BP300475 E
AL561509 A
AL561522 A
AK088815 N
BY199370 E
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BY181022 I
AV141507 P
BM922555 P
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Location/Qualifiers
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(c) 1993 - 2005 Compugen Ltd.
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Fgapop 6.0 , Fgapext
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Database

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Result

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/note="vector: mixed; The ORFs were PCR amplified from the MGC (Nammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR23 Donor vector. Reference: MGC (Nammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
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                                                                                                Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund May Smith 858, BOSTON, MA 02115, USA
1 Jimmy Fund May Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5180
Fax: 617 632 5180
Caris Construct. Each cloned ORF Casults From a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers
FORWARD: ATGGCTCAGCACCTA
BACKRARD: ATGGCTCAGCACCTA
TORWARD: ATGGCTCAGCATTTCATAGAT
TINGST Length: 608 Std Error: 55.00
Plate: 11032 row: 11 column: E
Seg primer: ACTGGCTGTTTTACAAGCTCGTGAAAAC
High quality sequence start: 91
High quality sequence start: 91
High quality sequence stop: 607
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Dricct, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro
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                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/tisme_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
Collection"
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Conservative:
Mismatches:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 608)
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     GTAAATATCCGAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAAACTCTGTT
                                                AlaTyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
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B. 1 (Bases 1 to 1074)

B. 1 (Bases 1 to 1074)

B. NIH-MGC http://mgc.nci.nih.gov/.

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: Louis Staudt, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

http://image.llni.gov

Plate: LiAM10068 row: b column: 14

High quality sequence stop: 638.
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/mol_type="mRNA"
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/clone="IMAGE:14385965"
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/clone lib="NIH MGC 85"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: Not!; Site 2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1:867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                   BG106937 1074 bp mRNA linear EST 30-JAN-2001
602291349F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4385965 5',
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                                                               361 ACCAAGGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGT
                                                                                                  LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
                                                                                                                                                      GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle
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                                                                                                                             TTAATGGCATCTGTGAACAGCACCTGTAATGTCACACTGACATGCTCTGTAGAAGAA
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1 (bases 1 to 582)

Suzuki, Y., Yamaahita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Squence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                     50 ATGCTCAGCACCACCTATGGATCTTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGC
1 MetalaGlnHis-HisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAl
                                                                                                                20 aGlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePr
                                                                                                                                                                                                                       OValAsnileGlnGluproArgGlnValLysileIleAlaTrpThrSerLysThrSerVa
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acttrccttaaatattcaagaaccaaagaaattgacaacattgcctgaacttctcaa 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 HisArgAsnTyrTyrGluArgileHisAlaLeuGlyProAsnTyrAsnLeuVallleSer 97
                                                                Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                      Table 1 to 923)
Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Iu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on allgament.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 TyrThrThrThrLygArgTyrAsnLeuGlnileTyrArgArgLeuGlyLygProLygile
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1 (bases 1 to 923)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                           /gene="CD84"
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TRANSCRIPT, partial sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CTTGGGAAACCAAAAATTACACAGAGTTTAATGGCATCTGTGAACAGCACCTGTAATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IlealaTrpThrSerLysThrSerValAlaTyrValThrProGlyAspSerGluThrAla
                                              /.organism="Homo sapiens"
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/cell type="macrophage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetPhePheLeuLeuValLeuIleLeuSerSerValPheLeu 245
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Matches:
Conservative:
Mismatches:
Indels:
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AY408983
           Email: ysuzuki@ims.u-tokyo.ac.jp.
   Location/Qualifiers
   1. .582
                                                                                                                                                                                                                                           Gaps:
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1008.00
100.00%
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Best Local Similarity:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 535)

Dias Neto,E., Garcia,Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.
                                                                                                                                                                                                                                                                                      90 GGAAGCGACACAGACATCTTCATAGTGAATGGGATTCTGGGGGAGTCAGCTATTCCC 149
                                                                                                                                                                                                                                                                                                                                                                                    150 TTAAATATCCAACCATCACAAAGTTACCATCATTTCTTGGCATTCCAAAACATCTGTT 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
                                                                                                                                                                                  MetAlaGlnHisHisLeuTrpIleLeuLeuCysLeuGlnThrTrpProGluAlaAla
                                                                                                                                                                                                                   ATGGCTCATCACCACCTATGGATCTTGCTTTTTGCCTACAAACCTGTCTGGAAGCAGC
                                                                                                                                                                                                                                                               GlyLyBAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 GCTTTCGTAAAACCAGGAAACTTTGGAGAAGAACCCATAGTTACCATAACCACCAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                            AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrTyrGluArgileHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg
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PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA,
BF754299 GI:12081079
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Mismatches:
Indels:
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  2.83e-90
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                    853.00
80.93%
69.07%
50.29%
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                                         Percent Similarity:
Best Local Similarity:
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                                                                               Query Match:
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VERSION
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S mith, T. P. L., Roberts, A. J., Echternkamp, S. E., Chitko-McKown, C.G., Wray, J. E. and Keele, J. W.

Wray, J. E. and Keele, J. W.

A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.
Plate: LAM8010 row: M column: 23
Seq primer: GTAATRACGACTACTAATRAGGG.
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                                           217
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114 AAGAAAACGGTATATGCTGTAGTT-----TCAAGAAATGCTCAACCCACAGAGTCCAGA 767
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  CTTCAAATCGTCCACTCCCCCATGGACCAAAAACTGACCTACACATGTACAGCCCAGAAC 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 ValTyrSerGluValGlnPheAlaAspLy8MetGlyLy8AlaSerThrGlnAspSerLy8 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mkNA"
/db xref="taxon:9913"
/tistue_type="mkNA"
/lab host="bH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pitultary, and
placenta/endometrium."
                                         ProvalSerAsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMet
                                                                                                                                                                                                                                                                                                                                                                  IleTyrAspGluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeulleLeuSerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSer
                                                                                                                                                                                                                                              654 CTCATTCCGATGTTGGCATTTCTGTTCCGTTTGTACAAGAGAAGGCGAGATGATGTCTCA
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                                                                                                                       218 GlyPheArgThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuVal
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/organism="Bos taurus"
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Bos taurus
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 7 CB467388 LOCUS

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

Alignment

ORIGIN

269 100 329

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20 89 40 389

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509 180 200 629 EST 10-JAN-2001 mRNA sequence.

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Percent Similarity:
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                                                                                                                                                                                                   Tel: +55-11-2704922

Razi: +55-11-270001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CT0547-
091000-001-a04&t3=2000-10-09&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence start: 7

High quality sequence stop: 533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSe 140
Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                    Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 lalatyrvalthrProGlyAspSerGluThrAlaProValValThrValThrHisArgAs
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Matches:
Conservative:
Mismatches:
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/organism="Homo sapiens"
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1. (Dases 1 to 837)

Suchi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamaaima,N. and Awata,T.

Okumura,N., Hamaaima,N. and Awata,T.

Okumura,N., Hamaaima,N. and Awata,T.

Okumura,N., Hamaaima,N. and Awata,T.

Okumura,N., Hamaaima,N. and Awata,T.

Okumura,N., Hamaaima,N. and Awata,T.

DEDE (Pig EST Data Explorer): construction of a database for ESTs derived from procine full-length oDNA libraries

Nucleic Acids Res. 32 (1), D484-D488 (2004)

Animal Genome Laboratory, Genome Research Department

National Institute of Agrobiological Sciences

2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan

Tel: +81-29-818-8627

Fax: +81-29-818-8627

Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute

Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="thymus"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
thymus"
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Low quality bases were trimmed based on the quality values.
                                                                                                                                                                                                                                                                                      BP159730 BP159730 ENTI-length enriched swine cDNA library, adult thymus Sus scrofa cDNA clone THY010074A04 5', mRNA sequence.
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rLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGl
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/organism="Sus scrofa"
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/db_xref="taxon:9823"
/clone="THY010074A04"
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                                                                                                                                                           160 uGluLysAsnValThrTyr 166
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BP159730.1 GI:40409203
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                                                          80
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Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Institute of Medical. Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysusuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
                 241 GCTGTTGTAGTACCAGGAAACTCAGGAACA-----ACGATACTGTAACCCACCAAAAT
                                                                                                                              GTCAGCAACAATTCTGACTCCATCTTGTGCCCCAGCAGCTCTGTGCAGACATCGCAGTGGGC
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                                                                                                               TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg
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                                                                                                                                                                                                                                                                                                    CGGAGTTTAATGACATCTATGAATGGCACCTGTAATGTCACACTGACATGCTCTGTGGAG
ValAsnileGinGiuProArgGinValiysileileAlaTrpThrSeriysThrSerVal
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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BP303194
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BIIS1764 1788 bp mRNA linear EST 05-JUL-2001
602915927F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5066478 5',
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 788)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTTATGTAACACCCAGGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCCACAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 TATTATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal-GluLysGl
                                                                                                                                                                                                                                                                                                                                                              MetalaGlnHisHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyLysAspSerGlullePheThrValAsnGlylleLeuGlyGluSerValThrPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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164
3
3
                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                (1-582)
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Mus musculus
                                                                                                                                                                                                                                                                                                              US-09-882-171-483 (1-329) x BP303194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI151764.1 GI:14611765
                                                                                                                                          2.83e-86
818.00
94.89%
93.18%
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5'-ATTCTAGAGGCCGAGGCGCGCAATACGGCCGGG-3' and 5'-ATTCTAGAGCCGAGGCGCGCAATTACGGCCGGG-3' and sriched library was constructed using the Clontech creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH MGC_127 and NIH MGC_128). Library created in the laboratory of T. Usbrary."
                                                                                                                                                                                                                          466 bp mRNA linear EST 18-OCT-2002
AGENCOURT 10434334 NIH MGC 126 Homo sapiens cDNA clone
IMAGE:6653558 5', mRNA sequence.
                                                     224 rGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeuSerSerValPh 244
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotaning Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 46)
NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466
1135
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                     eLeuPheArgLeuPheLysArgArgGlnAsp 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .466
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            BU927996.1 GI:24116726
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717.00
100.00%
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                     244
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SOURCE
ORGANISM
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DEFINITION
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                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                  BU927996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArgThrHisHisTh 224
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                                                                                                                                                                                            /db.xref="taxon:10090"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dibrary constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThriyrAsnirpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePheGlnThrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 TACCTICATATCTACCGTCGACTTAAAACACCAAAAATTACACAGAGTTTGATATCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccadgagtcaataaagctgaa-----gitaccataacccaggggggcacttataaaggacga
         ğ
 Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 07 plate: LLAM11179 row: e column: 07 High quality sequence stop: 782.
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151
36
59
6
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                       1. .788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-882-171-483 (1-329) x BI151764 (1-788)
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732.00
74.50%
60.16%
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Best Local Similarity:
Query Match:
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Pred. No.:
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genome Encyclopedia Project of Genome Exploration Research Genome Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell_type="NOD-derived CD11c +ve dendritic cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Veukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
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Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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                                                                                                                                                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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/strain="NOD"
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Nus musculus (house mouse)

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Analysis of the mouse transcriptome based on functional annotation
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NCI CGAP Subl library is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI CGAP Libraries. NCI CGAP CO4, NCI CGAP Pr28, NCI CGAP CO4, NCI CGAP Pr22, NCI CGAP LO10, NCI CGAP LO10, NCI CGAP LO10, NCI CGAP LO10, NCI CGAP LO10, NCI CGAP LO10, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI CGAP LU12, NCI 
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UI-H-BIO-aah-a-08-0-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone
IMAGE:2709039 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonuclectide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LINN at:
                                                                                                                                                                                                                                                                                                                                                                          140
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                                                                                                                                                                                                                                                                             TIAAATATTCAAGAACCAAAGAAATTGACAACATTGCCTGGACTTCTCAATCATCTGTT
                                                                                                                                                                                                             ThriysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer
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                                                                                          AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                                                                            |||:::::: |||||| ::::::
205 GCTTTTATAAAACCCAGGAGTCAATAAAGCTGAA-----GTTACCATAACCCAGGGCACT
                                                                                                                                                                                     TyrTyrGluArgileHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeuArg
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Homo sapiens
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(2.53.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                              ESSI.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 389)

SINI-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov/

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M. A.G. E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

Location/Obdilfiers

Lication/Obdilfiers
            UI-W./.
UI-HF-BMO-adu-d-01-0-UI.x1 NIH MGC_38 Homo sapiens cDNA clone
IMAGE:3062832 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
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Db 247 GAAATCCTGCAGTCCAAGGAAGAACACAGTGAACACAGTTTATTCC 306
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Oy 321 ThrSerSerTytGlulleVal 327
Db 367 ACTTCAAGCTTTGTG 387
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967 bp mRNA linear PRI 01-JAN-2000
Homo sapiens leukocyte differentiation antigen CD84 isoform CD84d
(CD84) mRNA, complete cds.
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AX224719 Sequence
BC020063 Homo sapi
CQ718714 Sequence
AJ723324 Homo sapi
AF054818 Homo sapi
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AC09143 Homo sapi
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CQ72314 Sequence
L42621 Homo sapien
AC18754 Homo sapien
AC18754 Homo sapien
AC18856 Rattus no
AC18856 Rattus no
AC18856 Rattus no
AC44129 Homo sapi
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BC074754 Homo sapi
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                          112632 H.sapiens m
17054816 Homo sapi
                                                                          U96627 Homo sapien
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/gene="CD84"
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-MODEL=frame+ p2n.model -DEV=xlh
-Q-Cgn2_1/USPTO_spool/US09882171/runat_04022005_114004_26025/app_query.fasta_1.910
-Q-Cgn2_1/USPTO_spool/US09882171/runat_04022005_114004_26025/app_query.fasta_1.910
-Q-Cgn2_1/USPTO_spool/US09882171/runat_04022005_114004_26025_0-LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=12 -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=500 - TRR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=bto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09882171 @CGN 1 1 4930 @runat_04022005_114004_26025_NCPU=6 -ICPU=3
-NOW MAAP -LARGEQUERY -NGG SCORES=0 -MATT -DSPBEOCK=100 -LONGLOG
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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CR541847 Homo sapi
AX474268 Sequence
U82988 Human leuko
                                                                                                                                                                                 February 5, 2005, 03:24:06; Search time 3491.17 Seconds (without alignments) 2761.994 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                           KDSEIFTVNGILGESVTFPV........NNSDSISARQLCADIAMGFR 199
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Compugen Ltd.
                                                                                                                                    nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4708233 segs, 24227607955 residues
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                                  GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                        AF054817
CR541847
AX474268
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Xgapop 10.0, Ygapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                              Sequence:
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No.
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www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD,
Contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence by full sequence check.
The last codon is followed by the 3' att site: GACCCAGCTTTCTT. att
The clone is validated by full sequence check.
Compared to the reference sequence NM 003874 (GI:4502686) we found
AA exchange(s) at position (first base of changed triplet):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Godon start=1
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/brotein id="CAG46645.1"
/brotein id="CAG46645.1"
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EKNYTYNMSPLGEEGNVLQTPGTPEDGELTYTCTAQNPVSNNSDSISARQLCADIAMG
FRTHHTGLLSYLAMPFLLVLILSSVFLFRERRRQDAASKKTIYTYINASRNYQPAES
RIYDEILQSKVLPSKEESVNTVXSEVQPADKMGKASTQDSKPPGTSSYEIV!"
                                                                                                                                                                                                                                                                                                                                                                                                       www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H0132D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                                                                                                       Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
                     Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J. Cloning of human full open reading frames in Gateway (TM) system
                                                                                                                                                                                               Hallack, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      880 (pro-sser)
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
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Mismatches:
Indels:
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Matches:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPDo834H0132D"
                                                                                                                                                                                                                                                                                                                                                                                    RZPD; RZPD0834H0132D, ORFNO 3790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lab host="DH5Alpha"
                                                                                                                          entry vector (pDONR201)
Unpublished
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Best Local Similarity:
Query Match:
DB:
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                       AUTHORS
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REFERENCE
                                                                                                                                                     JOURNAL
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/brotein_id="AAF21723.1"
/dx xxef="cid:6650110"
/translation="MAQHHAULLLLCLQTWPERAGKDSEIFTVNGILGESVTFPVNIQ
EPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRWE
BAGDYKADINTQADPYTTTRXTNLQYTRRLGGKPKTIOSLAMSYNSTCWTYTTCKSVEKE
EKNVTYNWSPLGEBEGNLQIFGPEDGELTYTCTAQNPSNNSDSISARQLGADIAMG
PRITHHTGLLSVLAMFFLLVLIISSVFLFRRRRQGASLQGRASEHSLFRSAVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRS41847 1inear PRI 29-JUN-2004 Homo sapiens full open reading frame CDNA clone RZPD0834H0132D for gene CD84, CD84 antigen (leukocyte antigen); complete cds, without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CR541847.1 GI:499456648
Full ORF shuttle clone, Gateway(TM), complete cds.
Homo sapiens (human)
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1 (bases 1 to 1040)

de la Fuente, M.A., Pizcueta, P., Nadal, M., Bosch, J. and Engel, P. CD84 leukocyte antigen is a new member of the Ig superfamily Blod 90 (6), 2398-2405 (1997)
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                        LysaspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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Human leukocyte antigen CD84 mRNA, complete cds.
U82988
US-09-882-171-483_COPY_22_220 (1-199) x AX474268 (1-1040)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                            21 AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla
                                                                                                                           41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                            1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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Cd2000 and cd2001 molecules and uses thereof
Cd2000 and cd2001 molecules and uses thereof
Patent: BP 1223218-A 29 17-JUL-2002;
Millennium Pharmaccuticals, Inc. (US)
Location/Qualifiers
1. .1040
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     US-09-882-171-483_COPY_22_220 (1-199) x CR541847 (1-984)
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                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (2008es 1 to 1067)
Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MRR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Marcelona 08036, Spain
Location/Qualifiers
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CD84c"
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42. .1028
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RIYDBILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKFPGTSSYEIVI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 CAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCCAGAACCCTGTCAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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Conservative:
Mismatches:
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Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118)
Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MAR-1998) Servel d'Immunologia, Hospital Clinic,
Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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CD84a"
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                                                                                  LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu
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Matches:
Conservative:
Mismatches:
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Percent Similarity:
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AF054816
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FRYHTMTGLLSVLAMPFELJVLLISSVFELFRERRRGGSGLNTFTKNSDSISARQLCADIANG
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MASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYSEVQFADKWGKASTQDSKRPGTSS
                                                                                                                                      HSLUACD84 1100 bp mRNA linear PRI 04-JAN-2002
H.sapiens mRNA for leukocyte differentiation antigen CD84.
Y12632
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                                                                                                                                                     S Gaya, A.
L. Unpublished
L. Unpublished
CE 2 (bases 1 to 1100)
SE 2 (bases 1 to 1100)
B Direct Submission
B Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Immunologia, Villarroel 170, Barcelona 08036, SPAIN
Location/Qualifiers
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133. .1086
/product="leukocyte differentiation antigen CD84"
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Corganiam="Homo sapiens"
/mol_type="mRNA"
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70.1089
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leukocyte differentiation antigen.
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/translation="MAOHHLWILLLCLQTWPBAAGKDSEIFTVNGILGESVTFPVNIO
BPRQVKIIAWTSKTSVAYVTPGDSETARVYTVTHRNYYERIHALGPNYNLVISDLRME
DAGDYKADINTQADPYTTTKRYNLQIYRRLGRFKITQSLMASVNSTCNVTLTCSVEKE
BRYTYTWSPLGEBGNVLQIPQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMG
FRTHHTGLLSVLAMFFLLVLILSSVFLFRERRQGRIFPEGKWWKLTFSPPGTFAIT
PRFS"
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Ruben, S.M., Rosen, C.A., Fischer, C.L., Soppet, D.R., Carter, K.C., Bednarik, D.P., Endress, G.A., Yu, G.L., N.J., Feng, P., Young, P.E., Greene, J.M., Ferrie, A.M., Duan, R., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y.,
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JP 2002510192-A/173.
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                                                                                                    Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 1299)

Palou, E., Freed, J.H., Sole, J., Pi, A., Vilella, A., Vives, J. and
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                                                                                                                                                                                            253 TATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAT
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                                                                                                                                                                                                                                              GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr
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                                                                            LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                             AsnileGinGluProArgGinValLysileIleAlaTrpThrSerLysThrSerValAla
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Direct Submission
Submitted (07-APR-1997) Servei Immunologia, Hospital Clinic,
Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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/ organisme="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/o. .912

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/o. odon_start=1

/codon_start=1

/product="CBB"AAD04232.1"

/db_xref="GI:4100319"
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PAT 17-JUL-2003

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186 human secreted proteins
Patent: EP 135296.2 A 174 15-OCT-2003;
HUMAN GENOME SCIENCES, INC. (US)
                                                                                  GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
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                              LysAspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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Mismatches:
Indels:
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Sequence 174 from Patent EP1352962.
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                                                      HUMAN GENOME SCIENCES INC
PN JP 2002510192-A/173
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PN JP 2002510192-A/173
PD 02-ARR-1990
PF 06-MAR-1997 US 60/040162,07-MAR-1997 US 60/040161 PR 07-MAR-1997 US 60/04038621,07-MAR-1997 US 60/040334 PR 07-MAR-1997 US 60/0403861,07-MAR-1997 US 60/040386 PI 07-MAR-1997 
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C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68,
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Matches:
Conservative:
Mismatches:
Indels:
Lafleur, D.W., Li, Y., Zeng, Z. and Kyaw, H. 186 human secreted proteins Parent: JP 2002510192-A 173 02-APR-2002, HUMAN GENOME SCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. 3173
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RIYDBILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDASKKTIYTINASRNTQPAES
Clone distribution: MGC clone distribution information can be fount through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 26 Row: o Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGACGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCACC
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                                                                                                                                                                                                                                                                                                                                                                                                         note="synonyms: SLAMF5, hCD84, mCD84, LY9B"
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/db_xref="G1:18043043".
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Matches:
Conservative:
Mismatches:
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Crissue type="Lymph, lymphoma"
Cclone_Iib="NIH MGC_85"
/lab_host="NHI08"
                                                                                                                                                                                                                                                                                                                                                'note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BC020063 3278 bp mRNA linear PRI 29-JUN-2004 Homo sapiens CD84 antigen (leukocyte antigen), mRNA (cDNA clone MGC:21324 IMAGE:4385965), complete cds.
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                                                                                                                                                           593
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Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCW-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contract: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                             533
                                                                                                                                                                                                        GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3278)
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Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                    181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
                                                                                                                                                                                                                                                                                                                               654 AATTCTGACTCCATCTGCCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 710
                                                                                                          141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
              MetalaSerValasnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu
                                          474 ATGGCATCTGTGAACAGCACCTGTAATGTCACACTGACATGCTCTGTAGAGAAGAAGAA
                                                                                                                                                           534 AAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGGTAATGTCCTTCAAATCTTC
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MGC.
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Homo sapiens
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                                                                          161 GInThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                                Krause, S.W., Rehli, W., Heinz, S., Ebner, R. and Andreesen, R. Characterization of MAX.3 antigen, a glycoprotein expressed on mature macrophages, dendritic cells and blood platelets: identity
                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                   181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe
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Submitted (05-FEB-1998) Krause S.W., Hematology, University of
Regensburg, Franz Josef Strauss Allee 11, Regensburg, D 93042,
                                                                                                                                                                                                                                                                                                                                                              AJ223324.1 GI:3392916
cell surface antigen; glycoprotein; MAX.3 antigen.
Homo sapiens (human)
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Homo sapiens mRNA for MAX.3 cell surface antigen.
AJ223324
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20164057
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Mammalia; Eutheria; Primates;
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Krause, S.W.
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Matches:
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Mismatches:
Indels:
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PE Corporation (NY) (US)
Location/Qualifiers
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CQ718714

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AF043445 1132 bp mRNA linear ROD 16-MAR-1999
Mus musculus CD84 leukocyte antigen (CD84) mRNA, complete cds.
AF043445
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                                                                                                                         1 LysaspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                     21 AsnileGlnGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerValAla
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                     3299
1999
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Homo sapiens
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                                        Percent Similarity:
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Query Match:
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Pred. No.:
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EPKKIDNIAWTSQSSVAFIKPGVNKAEVTITQGTYKGRIEIIDQKYDLVIRDLRMEDA
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GTYSKAPEPREKSNYLQIVHSPMDQKLTYTCTAQNPVSNSSDSVTVQQPCTDTPSFHPR
HAVLEGGLAVLFLLIIPMILAFLFRLYKRRRRIVLGEADDVSKKTYVAVVSRNAQPTE
SRIYDEIPQSKMLSCKKDPVTIIYSSVQLSEKMKETNMKDRSLPKALGNEIV"
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de la Fuence, M.A., Tovar, V., Pizcueta, P., Nadal, M., Bosch, J. and Engel, P.
Molecular cloning, characterization, and chromosomal localization of the mouse homologue of CD84, a member of the CD2 family of cell surface molecules
Immunogenetics 49 (4), 249-255 (1999)
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            Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                  2 (bases 1 to 1132)
de la Fuente, M.A., Tovar, V., Pizcueta, P. and Engel, P.
Direct Submission
Submitted (17-JAN-1998) Immunology Unit, Department of Cellular
Biology, Medical School, University of Barcelona, Casanova 143,
Barcelona 08036, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LyshapSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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238 TITATAAAACCAGGAGTCAATAAAGCTGAA-----GTIACCATAACCAGGGCACTTAT
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/product="CD84 leukocyte antigen"
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Matches:
Conservative:
Mismatches:
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/db xref="taxon:10090"
/chromosome="1"
/map="close to ly-9"
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/tissue type="macrophage"
1. 1132
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/db_xref="G1:4105143"
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musculus (house mouse)
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Search completed: February 5, 2005, 09:29:31 Job time : 3495.17 sec8

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Run on: ĕ

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Scoring table:

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Acd82804 cDNA segu
Adi2289 cDNA enco
Adi73891 thuman sec
Adi82906 thuman sec
Adi23392 PRO polyp
Adi72389 thuman sof
Acq23399 thuman sof
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Adi86363 DNA encod
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Add78173 Human Ly-
Add43598 Human CD2
Aad43601 Human CD2
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Aad439789 Hypoxia-i
Aad43978 Dendritic
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Ada40164 Human sec
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Aad43584 Human CD2
Aad63395 Human CD2
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AAL24045
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AAD63415
ABL89654
ADA40164
ADC73712
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AAD63414
AAD43596
ABV77939
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ADA56325
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ADL57104
ADK98595
ADL57102
ABS76363
AAS20420
ADO63781
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        Adol5707 Human leu
Adg19066 Human sof
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Abs73661 Human cDN
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                    version 5.1.6
- 2005 Compugen Ltd.
                                                                  nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Match Length DB
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Command line parameters:

Database

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                                                               LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
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                                                                                                           AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAAACCAAAAATTACACAGAGTTTA
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                                                                                                                                                                                                                                   LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe
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                                                                                                                                                  MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T cell; antiallergic; immunosuppressive; virucide; antibacterial; antiparasitic; cytostatic; gene therapy; human; gene; CD83; ds; leukocyte differentiation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte differentiation antigen CD84 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; SEQ ID NO 7; 161pp; English.
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09-OCT-2002; 2002US-0417243P.
18-OCT-2002; 2002US-041975FP.
08-NOV-2002; 2002US-04244777P.
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2002US-0417243P.
2002US-0419575P.
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kpression or activity of
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Jagged-1 or GPR-32)
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                                                                                                                                                                                                                                                                                                                                                                like domains and SLAM associated protein, termed CD2000 or CD2001, useful for treating immune, inflammatory, or hepatic circulatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 TATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
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                                                                                                                                                                                                                                                                                                                                            Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 AATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAAACATCTGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
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Mismatches:
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P-PSDB; AAE26238.
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Best Local Similarity:
                          EP1223218-A1
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Human soft tissue sarcoma-upregulated DNA - SEQ ID 1885.

26-AUG-2004 (first entry)

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relative to effector T cell function, or vice versa, in a subject. The method involves administering an agent that modulates the expression or activity of a molecule selected from PrGERS and TGFbetal, or Jagged-1, GPR-32, CD83, CD84, CD89, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-stamine R-H4, GPRS, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-related kinase to the subject, such that treatment occurs. The methods are useful for diagnosing, preventing or treating conditions characterized by a too-vigorous or weak effector T cell or regulatory T cell response to antigens associated with the condition, such as in an allergic response, an autoimmune disorder, a virsal infection, a microbial infection, a parasitic infection a tumour. The present sequence represents a DNA encoding a human leukocyte differentiation CD84 antigen, preferentially expressed in regulatory T cells.
from modulating the balance of regulatory T cell function
      benefits
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U; 0 Other; Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0

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GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
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LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal

US-09-882-171-483_COPY_22_220 (1-199) x ADQ19066 (1-1067)

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Length:
Matches:
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Mismatches:

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Alignment Scores:

AsnileGlnGluProkrgGlnValLygIleIleAlaTrpThrSerLysThrSerValAla TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 253 TATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAT TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100

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ADQ19066 standard; DNA; 1067

RESULT 3 ADQ19066 ADQ19066;

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sarcoma; cytostatic; gene therapy; vaccine; screening; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                        Zlotník A;
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                                                                                                                                                                                                                                                                                26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                                     (PROT-) PROTEIN DESIGN
                                                                                                                                                                                                                                                                                                                                                          Ginsburg WM,
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97US-0047492P.
97US-0047500P.
97US-0047500P.
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97US-0047503P.
97US-0047584P.
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      Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abrormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphom; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; ospitive disorder; schizzophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                             LysargTyrasnLeuGlnIleTyrargargLeuGlyLysBroLysIleThrGlnSerLeu 120
                                                                                                          Metalaservalasnserthrcysasnvalthrceuthrcysservalglulysgluglu 140
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                                                                                                                                                                                       Human secreted protein gene 164 clone HSAWF26.
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MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorder; Alzheimer's disease; infection; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional.
                                                                                                                                                                                         181 AsnSerAspSerIleSerAlaArgGInLeuCyaAlaAspIleAlaMetGlyPheArg 199
                                                                                                                                            LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                                               Human cDNA #1 for novel secreted protein gene 164.
                                                                                                                                                                                                                                                                                         ABS73661 standard; cDNA; 3173 BP
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97US-0040162P.
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07-MAR-1997;
07-MAR-1997;
11-APR-1997;
11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                       This sequence represents a nucleic acid molecule designated Gene 164 from the human cDNA clone HSAWF26 (deposited as clone ATCC 97903 and ATCC 209049) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. ANV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W7526) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polyputcleotides.

Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
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                                                                                                                                                Brewer LA;
                                                                                                                                    Greene JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
                                                                                                                                                                                                                                            New isolated human genes and the secreted polypeptide(s) they enuseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Gr
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R,
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;
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                     97US-0057761P.
97US-0058785P.
97US-0061060P.
           97US-0057669P
                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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P-PSDB; AAW74891.
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12-SEP-1997;
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA contess also given in the specification. The protein is used in a pharmaceutical composition use perification. The protein is used in a condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrowascular disorders e.g. cardiac arrest, cerebrowascular disorders e.g. cardiac arrest, cerebrowascular disorders e.g. cardiac arrest, cerebrowascular disorders e.g. cardiac arrest, or packets and fungi and ocular disorders infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The components. The present sequence capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a cDNA derived from a gene encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; dednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or seqdata.uspto.gov/sequence.html?DocID=6420526B1 Example 1; SEQ ID NO 174; 129pp; English. WPI; 2002-634796/68. P-PSDB; ABG95343. preservative.

BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other; Sequence 3173

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  Human; secreted protein; hyperproliferative disorder; leukaemia;

breast cancer; wound; reproductive disorder; blood-related disorder;

breast cancer; wound; reproductive disorder; blood-related disorder;

Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;

wiral infection; bacterial infection; fungal infection; AIDS; sepsis;

we renal disorder; kidney failure; cardiovascular disorder; cytostatic;

k angina pectoris; cerebral ischaemia; congenital heart defect;

respiratory disorder; neurological disorder; Alzheimer's disease;

minnusouppressive; antibacterial; haemostatic; thrombolytic;

anticoagulant; neuroprotective; thyromimetic; antiallergic;

matisthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;

matist manaron.
                     161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
 414 AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGTTTA 473
                                                                                                                                 cDNA sequence #164 containing coding region of a human secreted protein.
                                                                                                                                                              AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
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970S-0040336P.
970S-0040312P.
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970S-0043312P.
970S-0043314P.
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JSPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
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970S-0057650P.
970S-005761P.
970S-0058781P.
970S-005160P.
98WO-0050660P.
98WO-0019476.
                                                                                             GREENE J M.
FERRIE A M.
DUAN D R.
HU J.
FLORENCE K A.
OLSEN H S.
EISCHER C L.
EBNER R.
BREWER L A.
MOORE P A.
SAIT Y.
LAFLEUR D W.
                                           RUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
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YOUNG P.E.
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(ZENG/) ZENG Z.
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LysArgTyrAsnLeuGln11eTyrArgArgLeuGlyLysProLys11eThrGlnSerLeu 120
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP; Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM; Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R; Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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97US-0038621P. 97US-0040162P.

07-MAR-1997; 07-MAR-1997;

Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

18-JUN-2001; 2001US-00882171

US2003175858-A1.

18-SEP-2003

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9705-0040333P.
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The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding a
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Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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polypeptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer. The sequence encodes a novel human secreted protein of the invention.
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                                                                      Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;
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The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPS) they encode. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoletic disorders, candocrine disorders, diseases of the immune system, inflammatory in disorders and many others. Full details of disorders that may be prevented, diagnosed and/or treated by the above methods are given in the specification. The nucleic acid molecules may be used to produce their proteins. The nucleic acid and it's complementary sequences may also be used as DNA probbs in diagnostic assays to detect and quantitate the proteins and the proteins and adaptatic acids in samples, and therefore which the proteins may be in need of restorative therapy. The SPS may also be used as antigens in the production of antibodies adainst the production of antibodies adainst the production of antibodies and activity. The anti-SP antibodies may also be used to down regulate expression and activity. The anti-SP antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by represents a human secreted protein CDNA). The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z,
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22-AUG-1997;
22-AUG-1997;
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Bednarik DP; Greene JM, Ferrie AM; her CL, Ebner R;

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GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                                                                                                                                                                                               GluaspalaGlyaspTyrLysalaaspIleasnThrGlnalaaspProTyrThrThr 100
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                                                                                                                                                                                                                       TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
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                                                                                                                                                                                                                                       LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 LysargTyrasnLeuGlnIleTyrargargLeuGlyLysProLysIleThrGlnSerLeu
                                                                                                                               LysAspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                            AsnileGlnGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                        174 AATAICCAAGAACCACGGCAAGTIAAAAICATIGCTIGGACTICIAAAACAICGTIGCT
                                                                                                                                                                                                                                                                    TyrGluArglleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
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                                3173
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                                                                                                           US-09-882-171-483_COPY_22_220 (1-199) x ADH73891 (1-3173)
                                Length:
Matches:
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Mismatches:
Indels:
T; 0
 C; 712 G; 772
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  BP; 910 A; 773
                                 3.5e-105
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   Sequence 3173
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                       Alignment Scores:
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The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polyasaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, Burkitt's hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated heemolytic anaemia, myasthenia gravis, hypodremocorticism, glomerulonephritis, or anaemia, myasthenia gravis, hypodremocorticism, glomerulonephritis, or anaemia, myasthenia gravis, hypodremocorticism, glomerulonephritis, or anaemia, myasthenia gravis hypodaremocorticism, glomerulonephritis, or cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromsome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
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                                                                                                                                                                                                                       New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylltis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 TATGTAACACCAGGAGACTCAGAAACAGCACCGTAGTTACTGTGACCCACAGAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
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                                                                                                                      Wood WI;
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                                                                                                                      Schoenfeld JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening of therapeutically useful reagents.
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Conservative:
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Indels:
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                                                                                                                    Clark H, Dennis K,
                15-SEP-2003; 2003WO-US029097
                                                16-SEP-2002; 2002US-0411392P
                                                                                                                                                                        WPI; 2004-329389/30.
                                                                                (GETH ) GENENTECH
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121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140

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The invention relates to a novel isolated nucleic acid and the PRO
polypeptide encoded by it. A protein of the invention has
reliable interarchy, antiarthritic, antichematic, immunosuppressive,
cartinifiammatory, antiarthritic, antipsoriatic, antiallergic,
cateopathic, antidiabetic, dematological, antipsoriatic, antiallergic,
cateopathic, antidiabetic, and respiratory activity. A polynucleotide
contist, invention may have a use in gene therapy. The PRO polypeptide, its
cateomist, antagonist, or antibody that specifically binds to the
polypeptide is useful for treating an immune related disorder such as
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
invenile chronic arthritis, a spondyloarthropathy, systemic
cystemic inflammatory myopathy, Sjogren's syndrome, systemic
chrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
chisease, a demyelinating disease of the central or peripheral nervous
cystem, idiopathic demyelinating polyneuropathy, Gulllain-Barre syndrome,
a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
cdisease, infectious or autoimmune chronic active hepatitis, primary
bliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
                                                                                            587
                       527
                                                           160
                                                                                                                                   GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                                                     cadacrecreadedecaadedecreactracacereracaececagaacecrerereadaac 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                          AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
                                                                                                                                                                                                                               AATTCTGACTCCATCTCTGCCGGCAGCTCTGTGCAGACATCGCGATGGGCTTCCGT 704
LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                                                              Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide encoding cDNA SEQ ID NO:1120.
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                                                                                                                                                                                                                                                                                                                        ADP23942 standard; cDNA; 3299 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; immune system
                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark H, Schoenfeld J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                               9
inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autofimence or immune-mediated skin disease, abullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, ensemblaic premonary fibrosis, hypersensitivity pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                            40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABNSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
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                                                                                                                                                                                                                                                                                                                                                                                                             TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrGluarg1leHisAlaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArgMet
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                                                                                                                                                                                                                                                                                                      LysAspSerGlu11ePheThrValAsnGly11eLeuGlyGluSerValThrPheProVal
                                                                                                                                             Sequence 3299 BP; 956 A; 802 C; 750 G; 791 T; 0 U; 0 Other,
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Best Local Similarity:
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GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
                                                                                                                                                                                                                                                                                                                                                          Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by determining presence or absence of an allele of a linked polymorphic marker present on chromosome 1q22, were the marker is linked to a variant form of the SCZ gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was isolated using the method of the invention as the SCZ gene. This sequence has been previously identified as CD84, GenBank Accession No: NM 008874. CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. The proteins encoded by this sequence may be involved in the processes by which the brain responds to hiological stimuli. Therefore they may provide targets for therapeutic intervention in the treatment of Schizophrenia. The SCZ sequence may be used in a new method of diagnosing susceptibility to schizophrenia in a patient. The method comprises determining the presence or absence of an allale of a linked polymorphic marker in the DNA of the patient. The polymorphic marker is present in chromosome 1922 and is linked to a gene (SCZ) having a variant form associated with a phenotype of schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           orphic marker is present in chromosome 1922 and is linked to a gene
having a variant form associated with a phenotype of schizophrenia
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
allele; polymorphic marker; chromosome 1q22; ss
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                                                         Location/Qualifiers
45. .1031
/*tag= a
/product= "SCZ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 19; Page 68-70; 82pp; English.
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Best Local Similarity:
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Sequence 3326

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                                                                                                                                      LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyGluGlyAsnValLeuGlnIlePhe 160
                                                                                         MetalaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
                                                                                                                                                         GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
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                                                                                                                                                                                                                                                                                                                                                                                                                         soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                           AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
                                                                                                                                                                                                                                                           648 AATTCTGACTCCATCTGCCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 704
                                                     AAGGGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGTTTA
                                       LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu
                                                                                                       ATGGCATCTGTGAACAGCACCTGTAATGTCACACTGACATGCTCTGTAGAGAAGAAGAA
Human soft tissue sarcoma-upregulated DNA - SEQ ID 6219.
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                                                                                                                                                                                                                                                                                                        TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG
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                                                                                                                                                        LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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             Length:
Matches:
Conservative:
Mismatches:
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Alignment Scores:
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181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg
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                                                                                            ADL57104;
                                                  RESULT 14
                                                                       The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN/8851-ACN/9294 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     796 AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGTTTA
                                                                       otide associated with breast cancer, useful for polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                    3687. BP; 1073 A; 881 C; 838 G; 874 T; 0 U; 21 Other;
                                                                                                                                                                                                                                                                                                                                                                                                x ACN92105 (1-3687)
                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                         Novel isolated polypeptide associated with detecting presence of polypeptide in sample
                                                                                                                     Disclosure; SEQ ID NO 13255; 36pp; English.
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                            Wang Y, Steinmann
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         (MILL-) MILLENNIUM PHARM INC.
                                                WPI; 2003-787014/74.
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                            Xu Y,
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                            Lillie J,
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The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequences fully defined in the specification. A polypeptide of the invention has antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, virucide, antibacterial, fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, antiarthritic, antiarthritic, antiarthritic, antiarthritic, antiarthritic, antiarthritic, and antilpaemic activity. A polypotide of the invention may have a use in gene therapy. The polypeptides, nucleic acid molecules and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; gene; human; antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozozoaide; nootropic; neuroprotective; antiparkinsonian; protozozoaide; nootropic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antilipaemic; gene therapy; flbroblast growth factor receptor 4; FGFR4; complement factor i precursor; matrix metalloproteinase-15 precursor; MDC3; T-lymphocyte surface antigen Ly-9 precursor; flbroblast growth factor-21; FGF-21; antibha-2 macroglobulin-like polypeptide variant; antibekoproteinase 1 precursor; LiV-1; nuclear hormone receptor NOR-1; transmembrane protein-like; beta-necendorphin-dynorphin precursor.
1036 AATTCTGACTCCATCTCTGCCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
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10-SEP-2002; 2002US-0410320P.
16-SEP-2002; 2002US-041030P.
23-SEP-2002; 2002US-0411060P.
23-SEP-2002; 2002US-0412766P.
24-SEP-2002; 2002US-041276F.
25-SEP-2002; 2002US-0412767P.
36-SEP-2002; 2002US-0413342P.
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                                                                                                                                                                                                                                                                                                                                                                                                            Human NOV5b gene SEQ ID NO:49.
                                                                                                                                                                                          ADL57104 standard; DNA; 1581
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127 GCAGAGAAAAGTGTTCTGTACAGCTGGACCCCAAGGGAACCCCCATGCTTCTGAGTCCAAT

GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys ThralaglnasnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCys

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are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder.

The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases such as metabolic disorders, diabetes, obesity, infectious diseases (Viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (Kypertension, atherosoclerosis), neurodegenerative disorders, Alzheimer's disease, pellepsy, immune disorders Alzheimer's constitution, and various dyslipidaemias. The nucleic acids and polypeptides cathma, and various dyslipidaemias. The nucleic acids and polypeptides cathma, and various dyslipidaemias. The nucleic acids and polypeptides cathma, heamatopolesis, wound healing and andjoagenesis, in generation of antibodies that bind immunospecifically to NoVX substances for use in therapeutic or diagnostic methods. The nucleic cades are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The NoVX collections in NoV1a-1t show homology to cibroblast growth factor receptor (FGFR4); NOV2a shows homology to fibroblast growth factor receptor (FGFR4); NOV3a shows homology to fibroblast growth factor seceptor (FGFR4); NOV3a-7c show homology to fibroblast growth factor seceptor (FGFR4); NOV3a-7c show homology to fibroblast growth factor seceptor (FGFR2); NOV3a-7c show homology to fibroblast growth factor cecptor collypeptide variant; NOV9a-9s show homology to the present sequence on codes a NOV9 or shows homology to consider the present sequence encodes a NOVY or transmembrane protein-like; NOV12a-12c show homology to beta-necendorphin precursor. The present sequence encodes a NOVX polypeptide of the invention.
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ADK98595 standard; cDNA; 1723 BP

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RESULT 15

ADK98595

1581 77 41 70 14 5 Conservative: Mismatches: Indels: Length: Matches: Gaps: 4.73e-29 352.00 58.42% 38.12% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

Sequence 1581 BP; 422 A; 442 C; 397 G; 320 T; 0 U; 0 Other;

US-09-882-171-483_COPY_22_220 (1-199) x ADL57104 (1-1581)

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100 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr---Gln 118
                                                                                                                                                                                                                                                                                                                                                                  GAGGAGGAATTCACCCCTGTTCGTCTATGAGCAGCTGCAGGAGCCCCAAGTCACCATGAAG 366
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|TCTGTGAAGGTGTCTGAGACTTCTCCTGTAACATCACTCTAATGTGCTCCGTGAAGGGG 426
                                                                                                                                                                                                                                                                                                             306
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                                                                                                   82 AACATCTCAGTAGACACAGAGATTGAGAACGTCATCTGGATTGGTCCCAAAAATGCTCTT 141
                                                                                                                                                                                                                                          246
                                                                                                                                                                        GCTTTCGCACGTCCCAAAGAAAT------GTAACCATTATGGTCAAAAGC 186
                                                                                                                                                                                                        TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
                                                                                                                                                                                                                                                                             66
                                                                  AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSer---LysThrSerVal 39
                                                                                                                                     AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
                                AAGGACTICAGCCCCAACAGTGGTGTCAGGGATCCTAGGGGGTTCCGTGACTCTCCCCTA 81
                                                                                                                                                                                                                              crgaargargcaggarccracaaagcccagaraaaccaaaggaarrrgaagrcacacr
                                                                                                                                                                                                                                                                                                                                                                                                                  SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys
                                                                                                                                                                                                                                                                           MetGluaspalaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr
LysAspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluGluLysAsnValThrTyrAsnTrpSerProLeu-------
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The invention relates to a novel isolated immune response associated protein (IRAP) comprising any of 35 fully defined sequences given in the specification. The polypeptide of the invention demonstrates of antiatreriosclerotic, cytostatic, neuroprotective, antiparkinsonian, hepatotropic, cerebroprotective, antiinflammatory, nootropic and vasotropic activities and may be useful for treating a disease or condition associated with decreased expression or overexpression of functional immune response associated proteins, while the antibody is useful for diagnosing a condition or disease associated with the expression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease and Crohn's disease.

C Purthermore, the molecules of the invention may be utilised during gene therapy procedures. The current sequence is that of a human IRAP cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated immune response associated proteins (IRAP) polypeptide and polymucleotide, useful for diagnosing and/or treating disorders with aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TW;
SD;
                                                                                                                                                  cytostatic; neuroprotective; antiparkinsonian; hepatotropic; cerebroprotective; antiinflammatory; nootropic; vasotropic; arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease; Parkinson's; Crohn's; gene therapy; human; SS; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,, Elliott VS, Hafalia AJA, Richardson
Marquis JP, Chawla NK, Khare R, Becha
                                                                                                                                     antiarteriosclerotic;
                                                                                                Human immune response associated protein IRAP-23 cDNA.
                                                                                                                                       immune response associated protein; IRAP;
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                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-2002; 2002US-0407561P.
11.SEP-2002; 2002US-0410178P.
13-SEP-2002; 2002US-0410571P.
18-OCT-2002; 2002US-0419906P.
25-OCT-2002; 2002US-0421445P.
                                                                                                                                                                                                                                                                                                                                                            26-AUG-2003; 2003WO-US026988
                                                                    (first entry)
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                                ADK98595;
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100 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr---Gln 118
                                                                                                                                                                                                                                                                                                                           434 GAGGAGGAATTCACCCTGTCTATGAGCAGCTGCAGGAGCCCCAAGTCACCATGAAG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                    153 GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                173 ThralaginasnProvalSerAsnAsnSerAsp---SerIleSerAlaArgGinLeuCys 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 GCTTICGCACGTCCCAAAGAAAT-----GTAACCATTATGGTCAAAAGC 313
                                                                                                                                                                                                                                                                          80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 99
                                                                                                                                                       21 AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSer---LysThrSerVal 39
                                                                                                                                                                                             40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
U; 0 Other;
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                            Length:
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  Sequence 1723 BP; 456 A; 486 C;
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US-09-149-476-174

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Sequence 174, Application US/09149476

Petent No. 6420526

GENERAL INFORMATION:
TITLE OF INFORMATION:
FILE REPERRICE: P2002P1
CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040,162

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

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US-08-348-792-1
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US-08-80-8175-1
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            Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFTO_epool/USO9882171/runat_04022005_114004_26047/app_query.fasta_1.910
-Q=/cgn2_1/USFTO_epool/USO9882171/runat_D4FTX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRAR=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USO9882171_@CGN 1 1 93 @runat_04022005_114004_26047 -NCPU=6 -ICPU=3.
-NO MAAP -LARGEQUERY -NGG_CORES=0 -WAIT -DSPBLOCK=1100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TINEOUT=30 -TRIREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                      February 5, 2005, 06:13:46; Search time 134.551 Seconds (without alignments) 2420.040 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-227-357-53
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Maximum Match 100%
Listing first 45 summaries
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Database

Result No.

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Sequence

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EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056, 812

EARLIER PILING DATE: 1997-08-22

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Sequence 1456, Application US/09949016
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Best Local Similarity:
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Matches:
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Indels:
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-05
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US-09-949-016-1456

pequeuce 1430, Appitation US/USF37410
petent No. 6812339
GENERAL INFORMATION:
APPLICANT: VERYER, J. Craig et al.
APPLICANT: VERYER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOONI307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTWARE: PSESSEQ for Windows Version 4.0
SEQ ID NO 1456 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180 GluaspalaGlyaspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100 405 LysargTyrAsnLeuGlnlleTyrArgArgLeuGlyLyaProLys1leThrGlnSerLeu 120 Metalaservalasnserthrcysasnvalthrteuthrcysservalglutysgluglu 140 525 LysasnvalThrTyrasnTrpSerProLeuGlyGluGlydsnValLeuGlnIlePhe 160 165 40 9 80 21 AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr TyrGluarg11eHisAlaLeuGlyProAsnTyrAsnLeuVal11eSerAspLeuArgMet 346 GAAGACGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCACC US-09-882-171-483_COPY_22_220 (1-199) x US-09-949-016-1456 (1-3296) Conservative: Mismatches: Indels: Length: Matches: Gaps:

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RESULT 4

US-09-949-016-12299

i Sequence 12299, Application US/09949016

patent No. 6812339

GENERAL INFORMATION:
APPLICANT VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE-REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-30

PRIOR PELING DATE: 2000-10-63

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 13198, Application US/09949016
Sequence 13198, Application US/09949016
Sequence 13198, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CLO01307
CORRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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Conservative:
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Query Match:
DB:
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; ORGANISM: Human
US-09-949-016-12299
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Percent Similarity:
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                                   Sequence 557, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
PAPELICANT: WINTER, J. Craig et al.
APPLICANT: WINTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WINDER: 050/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-010-03
PRIOR FILING DATE: 2000-010-03
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                              US-09-949-016-557
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Pred. No.:
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8 ValAsnGly1leLeuGlyGluSerValThrPheProValAsnIleGlnGluProArgGln 27
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Matches:
Conservative:
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Indels:
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EARLIER FILING DATE: 1997-07-08
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EARLIER PELICATION NUMBER: 60/051,920
EARLIER PILING DATE: 1997-07-08
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EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
                                            PLICATION NUMBER: 60/051,916
LING DATE: 1997-07-08
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US-09-227-357-53
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrvalThrProGlyAspSerGluThrAlaProvalValThrValThrHisArgAsnTyr
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PC010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER FILING DATE: 1999-07-07
EARLIER PILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13198
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APPLICATION NUMBER: 60/051,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 53, Application US/09227357
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571.00
100.00%
99.09%
54.96%
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Query Match:
                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                   US-09-949-016-13198
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
                                                                           NAME/KEY:
LOCATION:
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                                                                                                          US-08-348-792-5
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US-08-462-738-5
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88 AlaAspIleAsnThrGlnAlaAspProTyrThrThrThrLysArgTyrAsnLeuGlnIle 107
                                                                                                                                                                                               4I1 GCTCAAGTCAACCTGAGAACATCCCAGATCTCTACCATGCAGCAGTACAATCTATGTGTC 470
                                                                                                                                                                                                                             108 TyrArgArgLeuGlyLys-ProLysileThrGlnSerLeuMetAlaSerValAsnSerTh 127
                                                                                                                                                                                                                                                                                                        531 CTGCAGTATGTCCCCTGGTGTGTCTCTGTGGAGRAAGGCAGGCATGGATATGACCTACAGCT 590
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                                                                                                                                                                                                                                                                                                                                                                                                                            rpSerProLeuGlyGlu------GluGlyAsnValLeuGlnIlePheG 161
                                                67
                                                                                                     68 GlyProAsnTyrAsnLeuVallleSerAspLeuArgMetGluAspAlaGlyAspTyrLys 87
                                                                                                                                                                                                                                                                                     127 rCysAsnValThrLeuThrCysSerValGlu-LysGluGluLysAsnValThrTyrAsnT
                                           48 GluThrAlaProValValThrValThrHisArgAsnTyrTyrGluArgIleHisAlaLeu
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
COMPANIESTEICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
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02-DEC-1994
V: 530
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Patent No. 5576423
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFRENCE/DOCKET NUMBER: DX04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
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US-08-348-792-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                 235 AGCATCCACATTGTCGTCACAATGGCAAAATCACTGGAGAACAGTGTCGAGAACAAAATA 294
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Patent No. 5977303

GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: BURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
TITLE OF CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                          US-09-882-171-483_COPY_22_220 (1-199) x US-08-348-792-5 (1-1020)
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Conservative:
Mismatches:
Indels:
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43.15%
25.38%
15.40%
                                                                    CDS
61..975
TOPOLOGY: linear MOLECULE TYPE: CDNA
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151 ---GlyGluGluGlyAsnValleuGlnIlePheGlnThrProGluAspGlnGluLeuThr 169
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Sequence 5, Application US/09199955
Sequence 5, Application US/09199955
Sequence 5, Application US/09199955
Sequence 5, Application US/09199955
Sequence 5, Application Constant Consta
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ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                    138 LysGluGluLysAsnValThrTyrAsnTrpSer
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
APPLICATION NUMBER: US 08/461,473
FILING DATE: 02-UNN-1995
ATTOMNG DATE: 02-DEC-1994
ATTOMNG CARDY INVERMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INPORMATION:
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901 California Avenue
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
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STRANDEDNESS: single
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MOLECULE TYPE: CDNA
FEATURE:
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STATE: California
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Best Local Similarity:
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; LOCATION:
US-09-199-955-5
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-199-955-5
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeuArg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
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                                                                                                                       COUNTRY: USA
ZIP: 94304-1104
COMPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:
TELEROMORIC CHARACTERISTICS:
TELEROMIN: 415-852-9196
TELECOMMUNICATION OF SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TELENTH: 1020 base pairs
TYPE: nucleic acid
STANDEDNESS: single
TYPE: nucleic acid
STANDEDNESS: single
FEARTHER: TYPE: CDNA
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Matches:
Conservative:
Mismatches:
Indels:
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901 California Avenue
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15.40%
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LOCATION: 61..975
                                             CITY: Palo Alto
STATE: California
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Best Local Similarity:
Query Match:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
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08/348,792
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                                              NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
                                                                                                                                                                                  LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
              FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
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43.15%
25.38%
15.40%
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APPLICATION NUMBER:
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Best Local Similarity:
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LOCATION:
US-08-880-875-5
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US-08-348-792-7
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                                                                                                                                                                                                                                                                                                                                           394 AAGGAGGATGAGGGATGGTACCTTATGACCCTG------GAGAAAAATGTTTCA 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 CCAGCCAACACTCCCCACCTCGTCCCTCGGCCCCCAGCATGCTGACAATATC 678
                                                                 TyrTyrGluArglleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
                                 ---ValAsnIleGlnGluProArg 26
                                                                                                   ---SerVal 39
                                                                                                                                                                     40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
                                                                                                                                                                                                                                                                                                           80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
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APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSer 186
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US-09-882-171-483_COPY_22_220 (1-199) x US-09-199-955-5 (1-1020)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
                                                                                                  27 GlnValLysIleIleAlaTrpThrSerLysThr----
                              12 LeuGlyGluSerValThrPhePro----
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08880875
Patent No. 6399065
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COMPUTER READABLE FORM:
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US-08-880-875-5
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                                                                                                                                   235 AGCATCCACATIGTCGTCACAATGGCAAAATCACTGGAGAACAGTGTCGAGAACAAAATA 294
                                                                                                                                                                                                                                                                                                                                                                                                         295 GTGTCTTCTTGATCCATCCGAAGCAGCCCTCCACGTTATCTAGGAGAAGTCGCTACAAGTTT 354
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                                                               LeuGlyGluSerValThrPhePro------ValAsnIleGlnGluProArg
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x US-08-880-875-5 (1-1020)
                                                                                                                                                                                                   27 GlnValLysileIleAlaTrpThrSerLysThr-------
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138 LysGluGluLysAsnValThrTyrAsnTrpSer--------ProLeu--- 150
                                                                                                                                                                                                                                                        151 --- GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 169
                                                                                                                                                                                                                                                                                                                                                  627 CCAGCCAACAGCTCCCACCTCTGACCTCCGGCCCCCAGCATGCTGACAATATC 686
                                                                        --GAGAAAATGTTTCA 449
                                                                                                                                                               100 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr
                                                                                                                                  118 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                   170 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSer 186
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08462738

Sequence 7, Application US/08462738

GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIN Release #1.0, Version #1.25
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-DE-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT NUMBER: DX0436GB
  102 AAGGAGGATGAGGGATGGTACCTTATGACCCTG---
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901 California Avenue
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TELEFAX: 415-496-1200
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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153..1073
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CITY: Palo Alto
STATE: California
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LOCATION:
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                        GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Ge Vries, Jan E.
TITLE OF INVENTION: FURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-882-171-483_COPY_22_220 (1-199) x US-08-348-792-7 (1-1079)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P:
REGISTRATION NUMBER: 34,090
REFRENCE/DOCKET NUMBER: 34,090
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 350
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENTH: 1.10.7 Dase pairs
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
ENDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
         Sequence 7, Application US/08348792
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160.00
43.15%
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TYPE: nucleic acid
STRANDEDNESS: single
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) LOCATION: 153..1073
US-08-348-792-7
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                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
CLASSIFFICATION:
CLASSIFFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REFENCE/DOCKET NUMBER: DX0436GC
TELEPHONE: 415-652-9196
                                                                                                                                                                                                                                                                      TELEPAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160.00
43.15%
25.38%
15.40%
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                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                             TYPE: nuclei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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DB:
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343 AGCATCCACATTGTCGTCACAATGGCAAAATCACTGGAGAACAGAGGAGAAAAA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-chun J.
APPLICANT: Chang, Chia-chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                     US-09-882-171-483_COPY_22_220 (1-199) x US-08-462-738-7 (1-1079)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 Length:
Matches:
Conservative:
Mismatches:
                                                                         Indels:
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STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09199955 Patent No. 6372899
                160.00
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                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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100 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 117
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363 TATCTGGAG-----AATCTCACCCTGGGGATACGGGAAGCAGG 401
243 AGCATCCACATTGTCGTCACAATGGCAAAATCACTGGAGAACAGTGTCGAGAACAAAATA 302
                                                                                  303 GTGTCTTTGATCCATCCGAAGCAGGCCCTCCACGTTATCTAGGAGATCGCTACAAGTTT 362
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                                            40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                                                                                           60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg
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; Patent No. 5576423
; GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Gek, Benjamin G.
APPLICANT: Gek, Benjamin G.
APPLICANT: Gevies, Jan B.
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INPORMATION:

NAME:

CLASSIFICATION NUMBER:

ATTORNEY/AGENT INPORMATION:

NAME:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

TELECOMMULICATION INFORMATION:

TELECOMMULICATION INFORMATION:

TELECOMMULICATION INFORMATION:

TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
WEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1716 base pairs
TYPE: nucleic acid
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STATE: California
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                                                           170 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSer 186
                                                                                                                                                                                                                                   APPLICANT: Aversa, Gregorio
APPLICANT: Cang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: SURPACE ANTIGENS, PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESSE: DNAK Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-882-171-483_COPY_22_220 (1-199) x US-08-880-875-7 (1-1079)
                                                                                                                                                                                                                                                                                                                                                                                                                                   COKRESPONDENCE ADDRESS:
COKRESPONDENCE ADDRESS:
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
CUNTRY: USA
ZUP: 94304-1104
COMPUTER: EDDPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
FILING DATE: 07-2010
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-2010
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-2010
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-2010
APPLICATION NUMBER: US 08/481,777
FILING DATE: US-DEC-1994
ATTCRNEY/AGENT INFORMATION:
NAME: Ching, Edwin P. REFERENCE/DOCKET NUMBER: DX0436K
TELEPRAX: 415-452-9196
TELEFRAX: 415-652-9106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                            Sequence 7, Application US/08880875
Patent No. 6399065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1079 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.42e-10
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15.40%
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; LOCATION: 153..1073
US-08-880-875-7
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Query Match:
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Pred. No.:
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175 TIGGGAAGCAAAGIGCTGCTGCCCCTGACAIAIGAAAGGAIAAAATAAGAGCAIGAACAAA 234
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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43.15%
25.38%
15.40%
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                          FEATURE:

NAME/KEY: CDS

LOCATION: 61..1065

US-08-348-792-1
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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Search completed: February 5, 2005, 11:31:57 Job time : 144.551 secs

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Description Sequence Sequence Sequence

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US-09-803-391-174

US-09-882-171-174

US-10-164-861-174

US-10-198-846-13255

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-QODBL=frame+ p2n. model -DEV=xlh
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRRT=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OOTFRT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=S509882171 @CGN 1 1 582 @runat 04022005 114005_26092
-NCPU=6 -ICPU=3 -NO MAAP -LARGEQUERY -NEG $20CRS=0 - WAIT -DSPBLOCK=100
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-FGAPOP=6 -PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                         February 5, 2005, 09:29:36; Search time 423.629 Seconds (without alignments) 2703.765 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
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     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                        nucleic search, using frame plus p2n model
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Maximum Match 100%
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Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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SUMMARIES

APPLICANT: FIRST Christopher C.
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
TITLE REFERENCE: 7853-244-99
CURRENT APPLICATION NUMBER: US/10/436,523
FRICH REPLICATION NUMBER: US/10/007,303
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PATENTING NUMBER: 09/706,167
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PATENTIN VERSION 3.1 ; sequence 29, Application US/10436523 ; Publication No. US20030180888A1 ; GENERAL INFORMATION: TYPE: DNA ORGANISM: Homo sapiens SEQ ID NO 29 LENGTH: 1040

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192
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; Sequence 174, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et 186
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFRENCE: P2002P2
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SEQ ID NO 174
; LENGTH: 3173
                                                                                                                                                                  US-09-882-171-483_COPY_22_220 (1-199) x US-10-723-860-1885 (1-1067)
                                                     1067
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3119)
OTHER INFORMATION: n equals a,t,g, or c
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Best Local Similarity:
Query Match:
DB:
   JS-10-723-860-1885
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US-09-809-391-174
                                   Alignment Scores:
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Publication No. US20040253606A1

GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION NUMBER: US/10/723,860

CURRENT APPLICATION NUMBER: US/10/723,860

PRIOR FILLING DATE: 2003-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARKE: PATENTION NUMBER: 60/429,739

PRIOR FILLING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SEQ ID NO 1885

LENGTH: 1067
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                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
                                                                           Percent Similarity:
Best Local Similarity:
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US-10-723-860-1885
                                Alignment Scores
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RETLING DATE: 1997-05-23

R RAPPLICATION NUMBER: 60/047,598

R PILING DATE: 1997-05-23

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R FILING DATE: 1997-05-23

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R APPLICATION NUMBER: 60/047,596

R PILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

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R RILING DATE: 1997-05-23

R RILING DATE: 1997-05-23

R RILING DATE: 1997-05-23

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/047,601

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,568

R FILING DATE: 1997-04-11
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RR APPLICATION NUMBER: 60/043,569

RR PILING DATE: 1997-04-11

RR FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,671

R APPLICATION NUMBER: 60/043,674
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R APPLICATION NUMBER: 60/047,583
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,617
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,618
                                                                                                      R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,334
R FILING DATE: 1997-03-07
R PILING DATE: 1997-03-07
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/043,669
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
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APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
                    FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,600
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Fublication No. US2003017585841
GENERAL INFORMATION:
TITLE OF INVENTION: 186 Human Secreted proteins
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
FRIOR FILING DATE: 2001-06-18
FRIOR FILING DATE: 1998-09-08
FRIOR PELICATION NUMBER: 09/149,476
FRIOR APPLICATION NUMBER: 09/149,476
FRIOR PELING DATE: 1998-09-08
FRIOR PELING DATE: 1998-03-06
FRIOR FILING DATE: 1998-03-06
FRIOR FILING DATE: 1998-03-06
FRIOR FILING DATE: 1998-03-06
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Conservative:
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; LOCATION: (3121)

; OTHER INDEMATION: n equals a,t,g, or

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MBER: 60/043,313 997-04-11 MBER: 60/043,672 997-04-11 997-04-11 997-04-11 MBER: 60/043,315 997-06-06 997-06-06 997-08-2 MBER: 60/056,886 997-08-2 997-08-2 MBER: 60/056,887	12. 10. 10. 10. 10. 10. 10. 10. 10. 10. 10	ER: 60/056, 63 ER: 60/056, 63 ER: 60/056, 84 ER: 60/056, 89 ER: 60/056, 89 ER: 60/057, 76 ER: 60/047, 59 ER: 60/047, 59 ER: 60/047, 59 ER: 60/047, 58 ER: 60/047, 58 ER: 60/047, 58 ER: 60/047, 58 ER: 60/047, 58 ER: 60/047, 58 ER: 60/047, 59 ER: 60/047, 58
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RESULT 6
US-10-723-860-6219
Sequence 6219, Application US/10723860
Publication No. US20040253606A1
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Watsaha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REPRENCE: 05882.0193.NPUS01
CURRENT FILING DATE: 2003-11-26
PRIOR PELING DATE: 2002-11-26
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6219
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                                                                                           MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
                                                                                                                                                               161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
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                                        LysArgTyrAsnLeuGlnileTyrArgArgLeuGlyLyAssProLysileThrGlnSerLeu
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NAME/KEY: misc feature
LOCATION: (2531)..(2547)
OTHER INFORMATION: n is
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ORGANISM: Homo Bapiens
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Best Local Similarity:
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                                                                                                                               21 ABNI1eGlnGlubroArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla 40
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        x US-10-164-861-174 (1-3173)
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publication No. US20030225248A1

GENERAL INFORMATION:

APPLICANT: ROBERTION:

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/10/164,861

CURRENT APPLICATION NUMBER: US/09/149,476

PRIOR APPLICATION NUMBER: US/09/149,476

PRIOR PILING DATE: 1998-09-08

PRIOR PILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-03-06

NUMBER OF SEQ ID NOS: 757

SEQ ID NO 174

LEARTH: 3173
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Matches:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3119)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: SITE
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US-10-164-861-174
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7500099CB1
US-10-471-449-20
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| Publication No. US2003009974A1
| GENERAL INFORMATION:
| APPLICANT: Lillie, James
| APPLICANT: Ku, Yongyao
| APPLICANT: Wang, Youzhen
| APPLICANT: Wang, Youzhen
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
| TITLE OF INVENTION: THERAPY OF BERAST CANCER
| TITLE OF INVENTION: THERAPY OF BERAST CANCER
| TITLE OF INVENTION: UNMBER: 06/306,220
| PRICR APPLICATION NUMBER: 60/306,220
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LOCATION: 1, 2, 3669, 3670, 3671, 3672, 3673, 3674, 3675, 3676,
LOCATION: 3678, 3679, 3680, 3681, 3682, 3683, 3684, 3685, 3686,
OTHER INFORMATION: n = A,T,C or G
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LENGTH: 3687
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Percent Similarity:
Best Local Similarity:
Query Match:
TYPE: DNA
ORGANISM: Homo
                      US-09-860-836B-12
                                                Alignment Scores:
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; Publication No. US20030054002A1
; GENERAL INFORMATION; WARD
; APPLICANT: WANDETAND, WARD
; APPLICANT: WANDETAND, WARD
; APPLICANT: WANDETAND, WARD
; TITLE OF INVENTION: IN IMMUNE TOLERANCE
; TITLE OF INVENTION: IN IMMUNE TOLERANCE
; TITLE OF INVENTION: US/09/860,836B
; CURRENT APPLICATION NUMBER: US/09/860,836B
; CURRENT APPLICATION NUMBER: US/09/860,836B
; PRIOR APPLICATION NUMBER: 60/204,963
; PRIOR PILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PATENTIN VEY: 2.1
; SEQ ID NO 12
; LENGTH: 2286
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           Length:
Matches:
Conservative:
Mismatches:
Indels:
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General information:
General information:
TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of TITLE OF INVENTION: that express Ly-9; TITLE OF INVENTION: that express Ly-9; CURRENT APPLICATION UNBER: US/10/310,612; CURRENT FILING DATE: 2002-12-04; NUMBER OF SEQ ID NOS: 2; SOFTWARE: Patentin version 3.1; SEQ ID NO 1.
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Matches:
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Indels:
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517 TCTGTGAAGGTGTCTGAAACTTCTGTAACATCACTCTAATGTGCTCCGTGAAGGGGGCA
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Publication No. US20030180888A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher C.
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF FILE REPERENCE: 7853-244-99
CURRENT APPLICATION NUMBER: US/10/436,523
PRIOR APPLICATION NUMBER: US/10/007,303
PRIOR PILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/706,167
                                                                                                                                                                                                            x US-10-328-538-1 (1-2448)
                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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           LENGTH: 2448
TYPE: DNA
ORGANISM: HOMO S
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Publication No. US20040109863A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of cells
TITLE OF INVENTION: that express Ly-9
FILE REFERENCE: HYS-68CP
CURRENT APPLICATION NUMBER: US/10/328,538
CURRENT FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 2
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577 GAGAAAAGTGTTCTGTACAGCTGGACCCCAAGGGAACCCCATGCTTCTGAGTCCAATGGA 636
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Matches:
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TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
FILE REPERENCE: 7883-244-999.
CURRENT APPLICATION NUMBER: US/10/436,523
CURRENT PILING DATE: 2003-05-12
PRIOR PILICATION NUMBER: US/10/007,303
PRIOR PILICATION NUMBER: 09/706,167
PRIOR PILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-03
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Publication No. US20030180888A1
GENERAL INFORMATION:
               NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
SEQ ID NO 84
LENGTH: 652
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332.00
58.56%
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31.95%
      PRIOR FILING DATE: 2000-11-03
                                                               TYPE: DNA
ORGANISM: Homo sapiens
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; Sequence 75, Application US/10436523
; Publication No. US2003018088A1
; GENERAL INFORMATION:
    APPLICANT: Fraser, Christopher C.
    TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF;
    FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2001-11-20
; PRIOR PILING DATE: 2001-11-20
; PRIOR FILING DATE: 2001-11-3
; RIOR FILING DATE: 2001-11-3
; NUMBER OF SEQ ID NOS: 100
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                                                   TYPE: DNA
ORGANISM: Homo sapiens
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; SEQ ID NO 93
; LENGTH: 870
; TYPE: DNA
; ORGANISM: HOMO 86
US-10-436-523-93
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US-10-436-523-93

i Sequence 93, Application US/10436523

j Sequence 93, Application Wo. 105.0030180888A1

j GENERAL INFORMATION:

i TITLE OF INVENTION:

TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

FILE REFERENCE: 7883-244-999

CURRENT APPLICATION NUMBER: US/10/436,523

CURRENT APPLICATION NUMBER: US/10/007,303

PRIOR PILING DATE: 2001-11-20

PRIOR PILING DATE: 2001-11-20

PRIOR FILING DATE: 2001-11-03

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin version 3.1
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SOFTWARE: PatentIn version
SEQ ID NO 75
LENGTH: 870
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                                              ORGANISM: Homo
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Clark, A.G. (Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., G. (Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tacabaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

L. Submitted (IG-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (IG-NOV-2003) A Section of Genomics of Genomic exons and ordering them based on alignment.

This sequence was made by sequencing genomic exons and ordering them based on alignment.

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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;

Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 987)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Homo sapiens CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
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BG243220 E
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AGG090451
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ALS974433
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CKS90888
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Copyright (c) 1993 - 2005 Compugen Ltd
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L. Science 302 (5652), 1960-1963 (2003)

Science 302 (5652), 1960-1963 (2003)

B. 2 (bases 1 to 987)

S. Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

L. Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Pan troglodytes CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 987)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
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Mismatches:
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Matches:
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AY408982.1 GI:39764950
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REPERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

CV023928

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BG106937 1074 bp mRNA linear EST 30-JAN-2001
602291349F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4385965 5',
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lunpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis Staudt, M.D., Ph.D.

Tissue Procurement: Louis Staudt, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

http://image.llh.gov

Plate: LLAM10068 row: b column: 14

High quality sequence stop: 638.

Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_88"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: Not1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrGluarg1leHisAlaLeuGlyProAsnTyrAsnLeuVal1leSerAspLeuArgMet
AsnileGinGluProArgGinValLysileIleAlaTrpThrSerLysThrSerValAla
                                                                                TyrvalThrProGlyAspSerGluThrAlaProvalvalThrValThrHisArgAsnTyr
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Donor vector. Reference : MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"
                                                                                                        CV023928 608 bp mRNA linear EST 20-AUG-2004 1001 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC020063, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 612 5739
Email: Marc_Vidal@dfci.harvard.edu
Forsulte from a PCR reaction using an MGC full-length cDNA as templace DNA and ORF specific primers
PCR PRimers
                                                                                                                                                                                                                                                                     Bukaryotza.

Mammalia; Butheria; Primates; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarthin; Hominidae; Homo.

I (bases I to 60 M.

Rual, J. F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,

Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,

Clingingsmith, T. Hariley, J. L., Esposito, D., Cheo, D., Moore, T.,

Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,

Vandenhaute, J., Cusick, M. E., Albala, J. S., Hill, D. E. and Vidal, M.

Genome Res. (2004) In press
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  FORWARD: ATGGCTCAGCACCAA
BACKWARD: ATGGCTCAATTCATAGCTTGAAGT
Insert Length: 608 Std Error: 55.00
Plate: 11032 row: 11 column: E
Seq primer: ACTGGCCGTCGTTTACAACGTCGTGAAAAC
High quality sequence start: 91
High quality sequence stop: 607
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Matches:
Conservative:
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535 bp mRNA linear EST 10-JAN-2001
PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA, mRNA sequence.
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BF754299.1 GI:12081079
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Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mzushina-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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                                                                                                                                                                                                                     macrophage"
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Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
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BP303350 GI:52232310
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Manalaia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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      Site 2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NIH_MGC Library."
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                                                                                            1074
186
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4
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                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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DEFINITION
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Pred. No.:
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Bukaryota; Bukaryota; Bukaryota; Bukaryota; Bukaryota; Bukaryota; Bovinae; Bos. Homes Bos. How 739)

En i (bases 1 to 739)

Smith, T.P. L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries and may, J.E. and Keele, J.W.

Outact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Wast Animal Research Center
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/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled From multiple tIssues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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                                                                                                                                  rLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLe
tGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrTh
                                         120 umetalaservalaanserThrCygAsnValThrLeuThrCysSerValGluLysGluGl
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/tisaue_type="pooled"
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AUTHORS
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VERSION
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CB467388
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/organism="Homo sapiens"
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/dev stage="Adult"
/dlone_lib="CT0547"
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                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (baees 1 to 535)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M. A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., G.Y., Soaree, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CTO547-
091000-001-a04&t3=2000-00.09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence start: 7
High quality sequence stop: 533.
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                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysAspSerGlu1lePheThrVal-AsnGly1leLeuGlyGluSerValThrPheProVa
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Mismatches:
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                           sapiens (human)
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Suina; Suidae; Sus.

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

E (bases 1 to 837)

Suchishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasima, N. and Awata, T. onstruction of a database for ESTs derived from porcine full-length cDNA libraries

Nucleic Acids Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan

Tel: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP159730 all-length enriched swine cDNA library, adult thymus Sus scroofs cDNA clone THY010074A04 5', mRNA sequence.
BP159730.1 GI:40409203
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Low quality bases were trimmed based on the quality values.
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                                                                                                                           Single pass sequencing of clones derived from oligo-capped cDNA library
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                                                                                                                                                                             AsnileGinGluProArgGinValLysIleIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                                                177 AATATCCAAGAACCACGCCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCT
                                                                                                                                                                                                                                                        TyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal-GluLysGluGl
                                                                                                   LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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BST project with full-length enriched cDNA libraries carried
Animal Genome Research Program (Japan) by National Institute
Agrobiological Sciences and STAFF-Institute
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quality bases were trimmed based on the quality values
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  67.08%
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous Block structure in the promoter regions Contact: Yutaka Suzuki
Department of Virology
                                                            61
                                                                                GluArgileHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMetGlu
                                                                                                                                                                                                                                                                                                               396 TCCTACAACTTCAAGTCTATCGTCGTCTTGAGAAGCCAAAAATTACTCAGAGTTTCGTG
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                                                        ValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyrTyr
                                                                                                                                                                                                                                                  336 GACTCAGGGATCTACAAAGCCGACATAAATGTAGAGACCTCTAAAGTGACGACCACCAGG
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/clone_lib="Sugano cDNA library, macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 SerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMet 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 TCTGACTCCATCTCTGCCCAGCAGCTCTGTGCAGACATCACAATG
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/db_xref="taxon:9606"
/clone="MPE07792"
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                 Tumor Gene Index
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       /mol_type="mRNA"
/db_xref="texon:9823"
/clone="THY010074A04"
/tissue_type="thymus"
/fev stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult thymus"
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                                                                                                                                                                                                                                                                                                                                                                                                                300
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                           22 ileGlnGluProArgGlnVallysIleIleAlaTrpThrSerLysThrSerValAlaTyr 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAla---AspProTyrThr--- 99
                                                                                                                                                                                                                                                                    AspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProValAsn 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW013969 10-SEP-1
UI-H-BIO-aah-a-08-0-UI.s1 NCI_CGAP_SUb1 Homo sapiens cDNA clone
IMAGE:2709039 3', mRNA sequence.
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Homo sapiens
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/clone_lib="Nci_CGAP_Suli"
/clone=libe="Vector: pi7130-Pac (Pharmacia) with a modified
/note="Vector: pi7130-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The
NCI CGAP Suli library is a subtracted library derived from
BI. BI Constitutes a mixture of 21 normalized or
subtracted NCI CGAP Pr28, NCI CGAP_CG10,
NCI CGAP_FC2, NCI CGAP PR28, NCI CGAP_CG10,
NCI CGAP_Exid; NCI CGAP_Kid1, NCI CGAP_LLI, NCI CGAP_LLI2,
NCI CGAP_Exid; NCI CGAP_Kid1, NCI CGAP_LLI4,
NCI CGAP_LLI9, NCI CGAP_Exid NCI CGAP_LLI4,
NCI CGAP_LLI9, NCI CGAP_Exid NCI CGAP_LLI4,
NCI CGAP_LLI9, NCI CGAP_Exid NCI CGAP_LLI4,
NCI CGAP_LLI9, NCI CGAP_GC4, NCI CGAP_LLI4,
NCI CGAP_LLI9, NCI CGAP_GC4, NCI CGAP_LLI4,
NCI CGAP_LLI9, NCI CGAP_GC4, NCI CGAP_LLI4,
NCI CGAP_LLI3, NCI CGAP_GC4, NCI CGAP_RAG as a tracer
in a subtractive hybridization with a driver whose
composition is detailed below: NCI CGAP_Ridd pool 1 LLAM
3334.3337, 362-3683, 3798-3803, 1722-3725, 3776-3778
(IMAGE ClonelDe 1323912-1325831, 1471368-1472903,
(IMAGE ClonelDe 1323912-1325831, 1471368-1472903,
1492104-1493255) NCI CGAP_LUS pool 1 LLAM 3575-3582,
3851-3854 (IMAGE ClonelDe 148420-4477991,
1520004-1522439) NCI CGAP_LUS pool 1 LLAM 3575-3582,
3716-3720, 3733-3735 (IMAGE ClonelDe
LLAM 2457-2459, 2758-2759, 3062-3608 (IMAGE CLONELDE
CLONELDE 1057416-1061255, 1144504-1145351) The resulting
subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996). Normalization and
Subtraction: Two Approaches TO Facilitate Gene Discovery.
Genome Research 6, 791-806.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dr track that was present in the
oligonuclectide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LINI. at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 AATGGGATTCTGGGGGAGTCAGTCACTTTCCCTGTAAATATCCAAGAACCACGCCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2709039"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402
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                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
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TAG_LIB=NCI_CGAP_Col0
TAG_SEQ=AAAGG"
                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Mus musculus (nouse mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 671)

2 (kazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A.,

Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, R.A., Frazer, K.S., Gasterland, T.,

Gariboddi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, D., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pevan, W.J., Pertea, G., Pesole, G.,

Ravasi, T., Reed, J. C., Reed, D. J., Reing, B. Z., Ringwald, M.,

Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B.Z., Ringwald, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 AAAGGACGAATAGAAATCATAGAAGTATGAAGTATGATCATTAGAGATG 251
                                                                                                                                                                                                                                                                                                                                                                                 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
                                                                                                                                                                                                                                                                                                                                                                                                         101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGhIlePhe 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 TTTATAAAACCAGGAGTCAATAAAGCTGAA-----GTTACCATAACCCAGGGCACTTAT 191
                                                                        AAAGATGCAGAACCCGATGGTAATGAATGGGATTCTTGGGGAGTCAGTTACTTTCCTCTTA
                                                                                                                              AsnileGlnGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 AAGATCTACCTTCATATCTACCGTCGACTTAAAACACCAAAAATTACACAGAGTTTG
                                           LysaspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                                                               41 TyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY748483 BIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus CDNA clone F630108106 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTICTGACTCTGTCACTGTCCAGCAGCCATGTACAGAC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAsp 193
  US-09-882-171-483_COPY_22_220 (1-199) x AY408983 (1-923)
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                                                                                                                                                                                                               163
89 AspileAsnThrGlnAlaAspProTyrThrThrThrLysArgTyrAsnLeuGlnIleTyr 108
                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                       109 ArgArgLeuGlyLysProLysIleThrGlnSerLeuMetAlaSerValAsnSerThrCys 128
                                                                                     68
                                                                                                                                                                     ProAsnTyrAsnLeuValIleSerAspLeuArgMetGluAspAlaGlyAspTyrLysAla 88
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inferring nonneutral evolution from human-chimp-mouse orthologous
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                222 CCGAACTACAATCTGGTCATTAGCGATCTGAGGATGGAAGACGCGCGGAGGAGTACTACAAAGCA
                                                                                                        282 ACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCCTTAGGT
                                                                                                                                                                                                                                                                                162 GACATAAATACACAGGCTGATCCCTACACCACCACCACGCATACAATCTAT
                                                                                                                                                                                                                                                                                                                                                                   102 CGTCGGCTTGGGAAACCAAAATTACACAGAGTTTAATGGCATCTGTGAACAGCACCTGT
                                                                                  49 ThralaProValValThrValThrHisArgAsnTyrTyrGluArg1leHisAlaLeuGly
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Conservative:
Mismatches:
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/gene="CD84"
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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EST 17-DEC-2002

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Mus musculus
Eukaryota; Macazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Butlandia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
I (bases 1 to 788)
Sull-MCC http://mgc.nci.nih.gov/.

I Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIIT79 row: e column: 07
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B1151764
B1151764.1 G1:14611765
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                                                                                                                                       :::::: ||||||| :::::: |||||| TITATAAAACCAGGGGACTTAT 261
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                                                                                                                                                                                                                                       GluaspalaglyaspTyrLysalaaspIleasnThrGlnalaaspProTyrThrThrThr
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                                                                                                                                                                                                                                                                                                               41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 AAGGATGTCACATATAGCTGGAGTCCCTTTGGAGAAAAAGCAATGTCCTTCAAATCGTC
                                                                                            LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAsp 193
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                                           US-09-882-171-483_COPY_22_220 (1-199) x BY748483
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Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wals, C., Wall, C., Wynshaw-Boris, A., Yanagiaswa, M., Yang, I., Yang, C., Wynshaw-Boris, A., Yanagiaswa, M., Yang, I., Yang, Z., Yang, I., Xonn, Z., Cavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Arakawa, T., Pukuda, S., Harai, T., Waki, K., Kawai, J., Alzawa, K., Arakawa, T., Pukuda, S., Harai, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Fire Institute of Empiritute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9226
Email: genome-resegnscriken.jp, URL:http://genome.gsc.riken.jp/Adachi,C., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Haysashida,K., Hirozane,T., Houri,F., Imotani,K., Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murate,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,M., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shitaki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Libract Submission
Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for trapper-selected CDNAs to prepare Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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/dol type="NoD"
/clone="F630108106"
/clone="F630108106"
/clone="F630108106"
/clone lib="RIKBN full-length enriched, NOD-derived CD11c
+ve dendritic cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
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Query Match: DB:

Pred. No.:

ORIGIN

FEATURES

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100

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MEDLINE PUBMED JOURNAL

COMMENT

TITLE

Euteleostomi;

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/tissue type="maxed (pool of 40 RNAs)"
/lab host="naxed (pool of 40 RNAs)"
/lab host="maxed (pool of 40 RNAs)"
/clonellb="NIH MGC_126"
/clonellb="NIH MGC_126"
/note="Vector: pDNR-infs, site 1: Sfil (ggccattatggcc);
Site 2: Sfil (ggccgcctcggcc); Double=stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.3%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'.AAGCAGTGGTATCAAGGAGGAGTGGCCATTACGGCCGGG-3' and 5'.ATTCTAGAGGCGAGGTGCTATTAGGGCCGACATGGTGT(30)NN-3'. Full-length enriched library was constructed using the Clontech creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH MGC_127 and NIH MGC_128). Library created in the laboratory of T. Library."
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                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capaba-ramail.nih.gov
Tissue Procurement: Nih.gov
Tissue Procurement: Nih.gov
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2903 row: m column: 14
High quality sequence stop: 437.
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                                                       1 (bases 1 to 466)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:6653558"
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AGENCOURT 10434334 NIH MGC 126 Homo sapiens cDNA clone
IMAGES653558 5', mRNA sequence.
                                                                                                                                /clone_lib="NCI_CGAP_Lu29"
//note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1;
//note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1;
//note="Organ: lung; Vector organization of the constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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                                                                         /tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
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Matches:
Conservative:
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57.51%
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Best Local Similarity:
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(dases I to 677)

(dases I to 677)

Lotoki, Y., Mattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submitssion

Submitted (O2-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbes@ger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS 03-NOV-2001
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                                                                                                                                  AGO90451 677 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-090A06.F, genomic survey sequence.
AGO90451
                                                                                                                                                                                                                            Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D.; Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
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                                                101 LysargTyrasnLeuGlnlleTyrargargLeuGlyLysPro 114
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Pred. No.:
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DB:
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81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
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8
                          61 TyrGluArg1leHisAlaLeuGlyProAenTyrAenLeuVal1leSerAspLeuArgMet
                                                                                                                                                                                    101 LysarglyrasnieuGlnileTyrargarg 110
                                                                                                                                                                                                                            516 AAGCGCTACAACCTGCACATCTATCGCAAG 545
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PK 07-MAR-1997 US 60/040162,07-MAR-1997 US 60/040133 PR 07-MAR-1997 US 60/040161 PR 07-MAR-1997 US 60/040161 PR 07-MAR-1997 US 60/040161 PR 07-MAR-1997 US 60/040163 PR 07-MAR-1997 US 60/040134 PR 07-MAR-1997 US 60/040163 PR 11-APR-1997 US 60/040163 PR 11-APR-1997 US 60/040163 PR 11-APR-1997 US 60/040163 PR 11-APR-1997 US 60/040163 PR 11-APR-1997 US 60/040163 PR 11-APR-1997 US 60/040163 PR 11-APR-1997 US 60/040163 PR STEVEN M RUBEN, CRAIG A ROSEN, CARRIE L FISCHER, DANIEL R SOPPET, PI KENNETH, CAPTER, DANIEL P BEDNARIK, GREGORY A ENDRESS, GUO LIANG PI YU, JIAN NI, PI THO FERO, PAUL E YOUNG, JOHN M GREENE, ANN PI JING SHAN HU, KIMBERLY A PLORENCE, HENRIK S OLSEN, REINHARD EBNER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI YI LI, ZHIZHEN ZENG, PC CLZNIS/12, C12NIS/12, C12NIS/12, C07KII4/47, C07KII6/18, C12QI/68, PC GOINN3/50, CC Strandedness Notes.
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PN JP 2002510192-A/173
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U96627 Homo sapien
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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		271	8.5		9	BD247970		BD2		8 F
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υ		3.6	4.5			AC023262		ACO	HOMO	gabı
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¥	AUTHORS	Rube	n, S.M	Ruben, S.M., Rosen, C.A.,	٦, ٥	A., Fischer, C.L.,		ppet, D.R.,	Soppet, D.R., Carter, K.C.,	
		Bedn	arik,	D.P., E	dre	Bednarik, D.P., Endress, G.A., Yu, G.L.,		N,J., Feng, P	Feng, P., Young, P.:	
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/product="MAX.3 cell surface antigen"
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Best Local Similarity 99.8%;
Matches 3160; Conservative
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108. .103
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  CTCTCCAGATGCACCATGCATGCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCCAG 2760
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                                                                                                                                                                                                                                                CACTGCTGTTTTTTCCTCTTTTGTCCTTCTATCACTAAAACTCATCTCATTCAGCCTTAC
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Direct Submission
Submitted (05-FBB-1998) Krause S.W., Hematology, University of
Regensburg, Franz Josef Strauss Allee 11, Regensburg, D 93042,
GERMANY
                                                                                                                                   TACCTCTTCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA
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                                              CCAGATGTGTGCCCCCACCCCATGTCCATTTACATGTCCTTCAATGCCCACCTCAAAAGG
                                                                       CCAGATGTGTGCCCCCCACCCCATGTCCATTACATGTCCTTCAATGCCCACCTCAAAAGG
                                                                                                                                                             TACCTCTTCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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cell surface antigen; glycoprotein; MAX.3 antigen.
Homo sapiens (human)
Homo sapiens
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="HDPFR19"
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QY 787 TCCGTTTGTTCAAGAGAGACAAGATGCTGCCTCAAAGAAAACCATATACCA 846 Db 781 TCCGTTTGTTCAAGAGAGAGAGTGCTGCTCAAAGAAAACCATATACATATATCA 840 QY 847 TGGCTTCAAGGAAACACCCAGCCAGCAGAGTCCAGAATCATGATGAAATCCTGCAGTCCA 906 Db 841 TGGCTTCAAGGAACACCCAGCCAGCAGAGTCCAGAATCTATGATGAAATCCTGCAGTCCA 900 QY 907 AGGTGCTTCCAAGGAACACCAGCAGTGAACACAGTTTATTCCGAAGTGCAGTCTG 966 Db AGGTGCTTCCCTCCAAGGAACAGCAGTAACACAGTTTATTCCGAAGTGCAGTCCTG 966	967 ATRAGATGGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGGACTTCAAGGT 	CCAATA CAATA	1087 CTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCAACTCTTACTGGGAGATTGCAAACT 1146 	AAACCTTCTGCTGGGCATAGCTTGTGCCTAAAACCTTCTGCTGAAAACCTTCTGCTGGGCATAGCTTGTGCCTAA		TAGCACATGTAGAAAATAATAT 1	TGACT 13	14	1447 ATATTTTGCACCCCGTAATAGGCCATGGCACACCAGCCAAGATGCTCTGCTCACACACA		GCAGA 	AIGHGGGCTGCATATAAGCACACTCATCCTTTGTCTGGGAATCTTTGTGCAGGGCATAA	TGTGG	CTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTTGGAAAATGTTCTTTCT	07 TCTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAGGATTTTC	T 19

	6.7 CTGACTTACAGGTGTACAGGTCGGAAACAGTGGACAACTGGACAACTCGTCGCC 666 6.5 CGGCACGTTACAGGACACTGGACTACTCGACACAACTCGACCAGGGTTGCTCAGC 6.6 CGGCACGTTGTGCAGACATCGCATCGACTACTCACCACGGGTTGCTCAGC 7.3 GTGCTGGCTACTTGTTCTCACTCTTCTCTCTCACACTGTTTTTTTT
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502686.
Location/Qualifiers
                  Strausberg, R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Submitted (19-DEC-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Center code: BCM-HGSC
Center code: BCM-HGSC
Center code: BCM-HGSC
Contact: angeborn.tmc.edu
Contact: angeborn.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                                                              WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CONA Library Preparation: Life Technologies, Inc.
CONA Library Prarayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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2341 TCCCAGTAAATGAATCCATAGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGA 2400	2427 GCTGCAAGGCCCCAAAGTAGAAGATGTGCATAATGTCTGCTCTTGTGTAGCTCAGGAGAC 2486 [2487 AATTCCAGCACAGAGACACTACAGTTAACGCTGAACTGCAGCTGCAAGTAATAGCATGAACA 2546	2547 GTCAGAAAATACCTTATGAGGGGGCAGGGCTGAAGCTGGGCCTTGAAGGATGGAT	2607 TTTGGATAGAGAATGAGGAGGACGTCCAAGTGAGAAGGATGAAAAATGAG 2666 	2667 AGGGGCCTGGATCAGTGGGGTGTATTCAGAGCACCTCTCCAGATGCACCATGCATG	2727 CAGTCCCTTGCCTATGTGTGGCAGAGTGTCCCCAGATGTGTGCCCCCACCCCATGTC 2786 [2787 CATTIACATGTCCTTCAATGCCCACCTCAAAGGTACCTCTTCTGTAAAGGTTTCCCTGG 2846	2847 TATCAGGAATCAAAATTAATCAGGGATCTTTTCACACTGCTGTTTTTTCCTCTTTTGGTCC 2906 2821 TATCAGGAATCAAAATTAATCAGGGATCTTTTCACACTGCTGTTTTTTTCCTCTTTTGGTCC 2880	2907. TTCTATCACTAAAACTCATCATCAGCCTTACAGCATAACTAATTATTTGTTTTCCTC 2966 1	2967 ACTACATTGTACATGTGGGAATTACAGATAACGGAAGCCKGCTGGGGTGGTGGCTCACG 3026 	3027 CCTGTAATCCCAACACTTTGGGAGGCCAAGGCAGGCGGATCACCTGAGGTCAGGARTTCG 3086	3087 AGATTARTCTGGCCAACATGGTGAAACCCCATNINIACTAAAAATACGAAATTAGCCAGG 3146 	3147 TGTGGTGGCACATCTGTAGTCCCAG 3173 	AL138930/c AL138930/c LOCUS AL138930 175386 bp DNA linear PRI 07-SEP-2001 DEFINITION Human DNA sequence from clone RP11-528G1 on chromosome 1, complete sequence. Requence.	ALL30930.13 GI:135946076 HTG. Homo sapiens (human) I Homo sapiens (all superioristical del superioristical	Mammalia; Butheria; Primates; Catarrhini; Hominidae, (bases 1 to 175386)	TITLE Direct Submission JOURNAL Submitted (07-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
<u>ස</u>	Qy Db	oy Oy	λο qα	çy qa	& A	<u>ک</u> ۾	\$ a	\$ a	QV DP	<u>ک</u> ۾	λο q _α	Qy Db	λό qa	RESULT AL1389 LOCUS DEFINI ACCESS	XEYWORDS SOURCE ORGANI	REFER	111 300
1287 CCAAACTICTTCCCAICAIAGCACAIGTAGAAAATAATATITITAIGGCACACIGGGAIA 1346 	AACAAGCAAGATTGCTCACTTCTGGAAGCTGCATATGACTAGAGGCCTCTTGTGACTGGA	GGTAACAACCCTGCCCAGTAACTGTGGGAGAGGGGATCAATATTTTGGACACCTGTAAT	AGGCCATGGCCACCAGGCCAAGATGCTCTGCTCACGTCAGTATGTGTGTG	AGGCA	1587 GATGCAGCCCTTCCCCCGAGTGCATGGCTTGGAGAGCAGAATGTGGGCTGCATATAAGCA 1646	CAAAC CAAAC	1707 ACAGATGACAGTGCTGTGGGTCTCTGTGAGTTGTGGCTCTCAGCCATGTAGACACA 1766	CTCTCCAAATGGAGTGTTGGAAAATGTTCTTTCTGCAGGTCTAGAGACTGCTGGGGCACAC	TTTTCTTGGAGTCCTACTTCAGAAGCCTTATAGGATTTTCTTTC	10100 	AACCA AACCA	TCAAATTAGAAGACCTTGCAAGAAGCAGAGTCATTCTCCAGAAGGAACTTGGGAGATGAT 	GGTGCAGATGATGAAACTGGGTTCATCCCAGTTCCAAAGACTCAGAGAACTAGAGTTTAA 	2127 GCTGAGGCAGCGCCACCCTGGCATGCCCCACAAACAGTCACCAGCCAG	ATCATTTAAGGAAGTGTTTCCCTTATGTGTTAGCAAGTATAATCGCCTAACTCCTAAATC	CCAATGAATAGTCCTAGGCTGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAG	2281 CCAATGAATAGTCCTAGGCTGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAG 2340 2367 TCCCAGTAAATGAATCCATAGACTCATCTAGCACCAACTACCATTAGGACTATGTTAGGA 2426

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requests: clonerequest@sanger.ac.uk
On Sep 10, 2001 this sequence version replaced gi:15021284.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP
database can be found at
http://www.sanger.ac.uk/Projects/Celegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1. constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/PGP/Chr1
RPI1-528G1 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: TWAPPARMP. THIS SPROTE Clone
TWAPPARMP. THIS SPROTE.
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Pred. No. 0;
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/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-528G1"
/clone="RP11-528G1"
31056. 31193
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Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequesr@sanger.ac.uk
On Aug 25, 2000 this sequence version replaced gi:9231058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 57% of reads
Chemistry: Dye-terminator Brancham; 42% of reads
Chemistry: Dye-terminator BT-amersham; 42% of reads
Chemistry: 170939 bases at least Q40
Consensus quality: 172842 bases at least Q30
Consensus quality: 173890 bases at least Q20
Insert size: 17569; sum-of-contigs
Insert size: 182579; 24.9% error; agarose-fp
Quality coverage: 5.06x in Q20 bases; sum-of-contigs Quality
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130504 131199: contig of 2696 bp in length
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11.176698
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clone_end:SP6
vector side:left"
8105. 11636
/note="assembly_fragment:01702
fragment_chain:1"
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Center code: SC
Web site: http://www.sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens chromosome 1 clone RP11-77110 map q21.3-23.1, 11
unordered pieces.
CAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCAATGGG 2339
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1020 TATGAAATTGTGATCTAGGCTGCTGGGCTGAATTCTCCCTCTGGAAACTGAGTTACAACC 1079
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                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
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gap of unknown length
contig of 30526 bp in length.
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/chromosome="11"
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Homo sapiens chromosome 01 clone RP11-566D7, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
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Submitted (28-OCT-1999) Genome Therapeutics Corporation, 100 Beaver
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                3000 GGAAGCCKGCTGGGGTGGTGGCTCACGCCTGTAATCCCAACACTTTGGGAGGCCAAGGCA
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On Aug 24, 2000 this sequence version replaced gi:8569080
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AC012471.7 GI:9887680
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
HOmo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7596905.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Center: Whitehead Institute/ MIT Center for Genome Research
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------ Project Information
Center project name: L8310
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 1, clone RP11-575N16
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SEQUENCE, 27 unordered pieces.
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Homo sapiens (human)
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 174880 bases at least Q40 Consensus quality: 182150 bases at least Q30 Consensus quality: 185136 bases at least Q20 Insert size: 176000; agarose-fp Insert size: 186457; aum-of-contigs Quality coverage: 4.5 in Q20 bases; sum-of-contigs Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
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3: gap of 100 bp
7: contig of 1266 bp in length
3: gap of 100 bp
7: contig of 1286 bp in length
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Qy 1200 TGCCTAAATGGACAAATGGATGCATACCCTTCCTGAAATGACTCCCTTCTGAATGAA	1260	1320	DD 99766 ATAATATTTTATGGCACACTGGGATAAACAAGGAAGATTGCTCACTTCTGGAAGGT	OY 1380 TATGACTAGAGGCCTCTTGTGACTGGAGGTAACAACCGTGCCCAGTAACTGTGGGAGAAG	99799	Db 99646 GGGATCAATATTTTGCACCTGTAATAGGCCATGGCACACCAGCCAAGATGCTCTGCTC	2y 1500 ACAGTCAGTATGTGTGAAGATCCCTGGTGCGTGGCCTTCACCACCATCTTGAGCAAATT	99586	Dy 1560 AddAAATGTACCCTTCGCTTGAGGCAGATGCACCCTTCCCCGAATGGATGG	1620	Db 99466 GAGCAGAAATGTGGGCTGCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGCAG	Oy 1680 GGCATAACAGGCTTAGTAAGTCCAAACACAGAGACAGTGCTGTGGGGTCTCTGTCAGA	99406	Oy 1740 GTTGTGGGTCTCAGCCATGTGGACACACTCTCCAAATGGAGGTTTGGAAAATGTTTTTCTTTC	1800	Db 99286 TGCAGGGTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAG		99226	by 1920 CAGCCATGCCCAGTATTCCCACTCTCCAAAAGAAACIGACCAGTTATATTCTCAAACAAAAGAAAAG	1980	90106 da	λο	7 Db 99046	DD 98986 CCAAAGACTCAGAGAACTTAAAGTTTAAAGTGAGAGAGTGCCGCCACGTGGCATGCCC	\dot 1	DD 98926 CACAAACAGAICACCAGCCAGCLIACACAGGAIIAACICICCCICAAIGAGGAACAGAACA	
FEATURES Location/Qualifiers 1189057 /ordaniam="Homo ganiens"	/mol type="general DNA" /mol type="general DNA" /db_xref="taxon:9606" /cfromosome="l" /man="l"		ragment	vector side:left" misc_feature 6762037	/note="assembly_tragment" misc_feature 21383255	/note="assembly_tragment" 33564509 /note="assembly fragment"	misc_feature 46105977 '- // note==assembly_fragment" misc_feature 6078 7083		/note="assembly_fragment" misc_feature 889810577 /note="ascembly fragment"		12044. /note="	misc_feature 1408315236 /note=massembly_fragment" 15177. 17412	-		misc_feature //loce="assembly_ragment" /note="assembly_fragment"		misc_teature 2449827225 /note="assembly_fragment" misc_feature 2732633481	/note feature 32582	<u>_</u> m-	017_11 agment.	core 2201.2; DB 2; Length 189057 red. No. 0;	ACTIVE 5; MISHIGACINES 6; INGELE 6; GAPS 7 AGATGGGGAAAGCCAGACACAGAAAACCTCCTGGGACTTCAAGC 101			113	100006 ACCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCACTCTTACTGGGAGATT 9994	1140 GCAAACTGCCACATCTCAGCCTGTAAGCAAAGCAGGAAACCTTCTGCTGGGCATAGCTTG 1190

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Homo sapiens leukocyte differentiation antigen CD84 isoform CD84c (CD84) mRNA, complete cds.
AP054815
AP054815.1 G1:6650105
                                                                                                                              Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1067)
                               LOCUS
DEFINITION
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KEYWORDS
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ORGANISM
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Palou, B., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20.MAR-1998) Servei d'Immunologia, Hospital Clinic,
Villarroel 170, Marcelona 08036, Spain
Location/Qualifiers
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255 GAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCCTTA 314 246 GAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCCTTA 315 246 GAAACAGCACCGGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCCTTA 305 315 GGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATGGAAGAGCGCAGAAGATCAAAA 374	426 TATCGTCGGCTTGGAAAATTACACAGAGTTTAATGGCATCTGTGAACAGCCC 485 495 TGTAATGTCACACTGACATGCTCTGTAGAAAGAAAGAAAG		855 ACGACACCAGCAGAGTCCAGAATCTATGATGAAATCCTGCAGTCCAAGGTGCTT 905 846 AGGAACACCCAGCCAGCAGAGTCCAGAATCTATGATGAAATCCTGCAGTCCAAGGTGCTT 905 915 CCCTCCAAGGAAGAGCCAGTGAACACAGTTTATTCCGAAGTGCAGTTTGCTGATAAGATG 974	HSUBLT 12 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB298 HSUB298 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB298 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB298 HSUB298 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB2988 HSUB298
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675 CGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGTACTCACCACCGGGTTGCT [Oy 855 AGGAACACCAGCAGAGAGTCCAGAATCTATGATGATATCTATGATGATCTAGATCTAGAGATCCAGAGTCCAGAGTCCAGAGAGTCCAGAGTCAGAGTCTAGATGATGAAATCTGATGAAATCTGAAGATCTAGAGAGTCTT 933 Db 874 AGGAACACCAGGAGAGTCCAGAATCTATTATTCCGAAGTGCAGTTTGCTGATAAGATG 974 Oy 975 GGGAAAGCCAGCAGAAGAACAAAACCTCCTGGGACTTTGCTGATAAAATTGTGATAGTG 993 Oy 975 GGGAAAGCCAGCACAAGGACAGTAAACCTCCTGGGACTTCAAGCTATGAAATTGTGATC 1034 Db 994 GGGAAAGCCAGCAACAAGAAAACCTCCTGGGACTTCAAGCTATGAAATTGTGATC 1053 Db 994 GGGAAAGCCAGCACAAGAAAACCTCCTGGGACTTCAAGCTATGAAATTGTGATC 1053	QY 1035 TAGGCTGCTGGGGT 1048 Db 1054 TAGGCTGCTGGGCT 1067 Db 1054 TAGGCTGCTGGGCT 1067 RESULT 11 AX474268 AX474268 AX474268 LOCUS DEFINITION Sequence 29 from Patent EP1223218. ACCESSION AX474268. AX474268.1 GRESION AX474268.1 GI:22213881 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (but apage) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Primates, Catarrhin lecules and uses th 129 17-UL-2002; tricals, Inc. (US) nalifiers Homo sapiens" 'unassigned DNA" axon:9606" axon:9606" ; Score 1033.4; DB ; pred. No. 6.9e-29 0; Mismatches	

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
CTGACTTACACGTGTACAGCCCAGAACCCTGTCAGCAACAATTCTGACTCCATCTCTGCC
                                                                                                                                        GRIGCTGGCTATGTTCTTTCTTGTTCTCATTCTTTTCAGTGTTTTTTGTTCCGTTTTG
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                                                                                                          GTGCTGGCTATGTTCTTTCTGGCTTGTTCTCATTCTGTCTTCAGTGTTTTGTTCCGTTTTG
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H.sapiens mRNA for leukocyte differentiation antigen CD84.
Y12632
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Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Immunologia, Villarroel 170, Barcelona 08036, SPAIN
Location/Qualifiers
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70. .1089
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leukocyte differentiation antigen.
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Unpublished
2 (bases 1 to 1100)
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DEFINITION
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AUTHORS
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AUTHORS
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JOURNAL
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FRTHHTGLLSVLAMFFLLVLILSSVEFERFRRRQDAASKKTIYTYIYAKSRNTQPAES
RIYDEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDASKESYEIVI"
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               2 (bases 1 to 1040)
de la Fuente, M.A., Pizcueta, P. and Engel, P.
Direct Submission
Submitted (21-DEC-1996) Hepatology, Fundacio Clinic, Villarroel
170, Barcelona 08036, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGAGATGGCTCAGCACCACCCTATGGATC
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42. .1028
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                                                                                                                                                                                                                                                            product="leukocyte antigen CD84"
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db_xref="G1:2618740"
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Pred. No. 6.9e-295;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 1034; Conservative
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This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.

This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.

This CDS has been cloned without stopcodon.

The CDS has been inserted into pDONR2Ol via a BP Clonase(TM)

reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GCT TCC ACC (ATG).

The last codon is followed by the 3' att site: GACCCAGCTTTCTT. att

The clone is validated by full sequence check.

Compared to the reference sequence NM 003874 (GI:4502686) we found
AA exchange(s) at position (first base of changed triplet):

880(pro->ser)
                                                                                                                                                                         CR541847 linear PRI 29-JUN-2004
Homo sapiens full open reading frame cDNA clone RZPDo834H0132D for
gene CD84, CD84 antigen (leukocyte antigen); complete cd8, without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Germany
RZPD, R.ZPD0834H0132D, ORFNO 3790
WWW.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H0132D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
GTTTATTCCGAAGTGCAGTTTGCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTAAA 1053
                                                                                                                                                                                                                                                                                                                                       Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 984)

Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S.,

Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,

Korn, B., Zuo, D., Hu, Y. and LaBaer, J.

Cloning of human full open reading frames in Gateway (TM) system
entry vector (pDoNR201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
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/clone=lib="Human Pull ORF Clones Gateway(TM) - RZPD"
/lab host="DHSAlpha"
/note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.zzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 984)
Halleck, Bertt, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstran, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
                                                                              1100
                                       Gateway (TM), complete cds
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CR541847
CR541847.1 GI:49456648
Full ORF shuttle clone, G
Homo sapiens (human)
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                                                                                                         Gaps
      /product="leukocyte differentiation antigen CD84"
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                                                                 31.2%; Score 991; DB 9; L. llarity 96.9%; Pred. No. 2.7e-282; Conservative 0; Mismatches 0;
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Catarrhini, Hominidae, Homo.
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       GAAATCCTGCAGTCCAAGGTGCTTCCCTCCAAGGAAGAGCCAGTGAACACAGTTTATTCC
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                                                                                                 TTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGCTGGAAAAGACTCAGAAATCTTCACA
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Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
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CD84#
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/organism="Homo sapien:
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/db_xref="taxon:9606"
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RIYDBILQSKVLPSRKBESVNTVYSSVQFADKNGKASTQDSKPPGTSSYEIVI
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31.0%; Score 982.4; DB 9;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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This sequence represents a nucleic acid molecule designated Gene 164 from the human cDNA clone HSAWF26 (deposited as clone ATCC 97903 and ATCC 209049) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV5951-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polynucleotides, by Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for
                                                                                                                                                                                                                   Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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                                                     AGCTGGCCCTTGAAGGATGGATGAATTTGGATAGAGAATGAGAAGACAGAGGCCTCC
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Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; Carter KC;

New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or preservative.

Example 1; SEQ ID NO 174; 129pp; English.

The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 CDNA seguences also given in the specification. The protein is used in a condition in the specification. The protein is used in a condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, crebrovascular disorders e.g. cardiac arrest, crebrovascular disorders infections caused by bacteria, viruses and fungi and ocular disorders (infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to alwoound culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The collures an also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a cDNA derived from a gene encoding one of the novel human secteted proteins of the invention. Note: This sequence did not form part of the printed specification, but was conditions and the condition of the movel human sected professed to the preservation of the preservation of the preservation of the preservation of the preservation of the printed specification, but was conditions and the conditions of the movel human sected professed to the preservation of the preservation of the preservation of the preservation of the preservation of the preservation of the preservation of the preservation of the preservation of the preservation of the preservation of the preservation of the prese seqdata.uspto.gov/sequence.html?DocID=6420526B1

Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Query Match 99.9%; Score 3169.4; Best Local Similarity 100.0%; Pred. No. 0; Matches 3173; Conservative 0; Mismatches

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(FERK/)
Human, secreted protein; hyperproliferative disorder; leukaemia;

Wreast cancer; wound; reproductive disorder; blood-related disorder;

Maemobnila; thrombocytopaenia; immunodeficiency; thymic hypoplasia;

W Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

Graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;

W viral infection; bacterial infection; fungal infection; AIDS; sepsis;

W angina pectoris; cerebral ischaemia; congenital heart defect;

R angina pectoris; cerebral ischaemia; congenital heart defect;

R angina pectoris; cerebral ischaemia; congenital heart defect;

R angina pectoris; carebral ischaemia; congenital heart defect;

R angina pectoris; cerebral ischaemia; congenital heart defect;

R antinacy disease; inflammation; Crohn's disease;

M munosuppressive; antibacterial; haemostatic; thrombolytic;

M anticasulant; neuroprotective; thyromimetic; antiallergic;

M cerebroprotective; cardiant; nootropic; antianginal;

M cerebroprotective; cardiant; nootropic; antiparkinsonian;
                         cDNA sequence #164 containing coding region of a human secreted protein.
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97US-0040162P
97US-0040334P
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ACD82641ACD82950 encode human secreted proteins or their fragments. Or specification, but was obtained in electronic format directly from the consorting and proteins or their fragments.
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    Rosen CA, Soppet DR, Carter KC
GA, Yu G, Ni J, Feng P, Young P
Hu J, Florence KA, Olsen HS, F
Moore PA, Shi Y, Lafleur DW,

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                          Claim 4; SEQ ID NO 174; 260pp; English.
CLSEN'H S.
FISCHER C L.
EBNER R.
BREWER L A.
MOORE P A.
SHI Y.
LAFLEUR D W.
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Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PB. Greene JM,
Duan DR, Hu J, Florene RS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                22-AUG-1997; 97US-0056881P.
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(ROSE) ROSEN C A.
(SOPP/) CARTER K C.
(BEDN/) ENDRESS G A.
(YUGG/) YU G.
(NIJA/) NI J.
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New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer.

Claim 1; SEQ ID NO 174; 256pp; English.

ø The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynuclectide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the cDNA sequence; a polynucleotide sequence encoding a polypeptide, or its fragment, domain, epitope or species homologue; or polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a

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er CL, Ebner R;
Y, Zeng Z, Kyaw H;
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Moore PA, Shi Y, Lafleur DW, Li Y,
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The invention relates to isolated nucleic acid molecules and the human

cc secreted proteins (SPB) they encode. The proteins and nucleic acids may come used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoletic disorders, cancer, haematopoletic disorders, diseases of the immune system, inflammatory confered disorders diseases of the immune system, inflammatory and disorders and many others. Full details of disorders that may be confered disorders and/or treated by the above methods are given in the proteins. The nucleic acid and it's complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the proteins. The nucleic acids in samples, and therefore which confined as an tigens in the production of antibodies against the proteins and in a sasays to identify modulators of SP expression and activity. The anti-SP antibodies may also be used to down regulate expression and activity. The anti-SP antibodies may also be used as diagnostic according the presence of the proteins in samples (e.g. by conzyme linked immunosorbant assay (ELISA)). The present sequence ö 9 540 600 9 99 720 720 GGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATGGAAGACG 360 420 420 480 480 61 ACCACCTATGGATCTTGCTTCCTTGCAAACCTGGCCGGAAGCAGCTGGAAAAGACT 120 CACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAAC 300 9 ACTCCATCTCTGCCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGTACTCGCCACAACAACACATCGCCTTCCGTACTCGCCACCACAACATGGCCATCTCCGTACTCGCCACAA GGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATGGAAGGACG Accacchanganchnechchrungchechaacchegeegaagcagcheaaaagach TGACATACAATTGGAGTCCCCTGGGAGAGAGGGGTAATGTCCTTCAAATCTTCCAGACTC TGACATACAATTGGAGTCCCCTGGGAGAAGAGGTAATGTCCTTCAAATGTTCTTCCAGACTC CTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGCAACAATTCTG 1 TCGACCCCASGCGTCCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGC AAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCTTATGTAA CAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCACCAAGCGCT ACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGTTTAATGGCAT TCGACCCCASGCGTCCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGC Gaps DB 12; Length 3173; ö Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other; 0; Indels 99.9%; Score 3169.4; 100.0%; Pred. No. 0; 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 3173; Conservative 241 361 .601 61 181 181 301 421 481 541 601 661 121 241 301 361 421 481 541 Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective 19A deficiency, selective 19M deficiency, selective 19M deficiency, selective 19M selective 19M transient hypogammaglobulinemia of infancy, Burkit's lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic ansemia, mysathenia gravis, hypodrenocorticism, glomerulonophritis, or ansemia, mysathenia gravis, hypodrenocorticism, glomerulonophritis, or ansemia, mysathenia gravis, hypodarenocorticism, glomerulonophritis, or ansemia, mysathenia gravis, hypodarenocorticism, glomerulonophritis, or or encer or immune-mediated inflammatory diseases. The PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development
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      2940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic; Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer; immune-mediated inflammatory disease; human; gene; ss.
     GAAGCCKGCTGGGGTGGCTGCCTCACGCCTGTAATCCCAACACTTTGGGAGGCCAAGGCAG
                                                                                                                                                                                    GCGGATCACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGGTGAAACCCCATNT
                                   AGCATAACTAATTATTTGTTTTCCTCACTACATTGTACATGTGGGAATTACAGATAAACG
                                                    GAAGCCKGCTGGGGTGGTGGCTCACGCCTGTAATCCCAACACTTTGGGAGGCCAAGGCAG
                                                                                                                                                                GCGGATCACCTGAGGARTTCGAGATTARTCTGGCCAACATGGTGAAACCCCCATNT
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                                                                                                                                                                                                                                NTACTAAAAATACGAAATTAGCCAGGTGTGGTGGCACACATCTGTAGTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 108; 695pp; English.
                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO24934 cDNA, SEQ ID 108.
                                                                                                                                                                                                                                                                                                                                                ADL82906 standard; cDNA; 3299
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Wu TD;
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ADL82906
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දු දු	1087 CTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTGCAAACT 1146	<i>k</i> 8	
දු දු	1147 GCCACATCTCAGCCTGTAAGCAAAGCAGGAAACCTTCTGCTGGGCATAGCTTGTGCCTAA 1206	<i>ኢ</i> 8	2227 CTGAGGAAGACATTCATATGATCATTTAAGGAAGTGTTTCCCTTATGTGTTAGCAAGTAT 2286
op Op	ATGGACAAATGGATGCATACCCTTCCTGAAATGACTCCCTTCTGAATGATGACAAAGGAATGGAAAAGGATGCCTTCTGAATGAA	<i>S</i> &	2287 AATGGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCAATGGGCTGCAAT 2346
S S	GGTTACCTAGTATAGTTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAATAATAT 13	S d	TAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCATAGACTCATCTAGCACCAACTA
oy D	1327 TTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCATATGACT 1386 	<i>ò</i> a	2407 CCATTAGCACTATGTTAGGAGCTGCAAGGCCCCCAAAGTAGAAGATGTGCGTAATGTCTGC 2466 [
\(\delta \)	AGAGGCCTCTTGTGACTGGAGGTAACCCTGCCCAGTAACTGTGGGAGAGAGGGATCA 	ò a	2467 TCTTGTGTAGCTCAGGAGACAATTCCAGCACAGACACTTAACGCTGAACTGCAGC 2526
දු දු	APAITTTGCACACCTGTAATAGGCCATGGCACCACCAGCCAAGTGTCTCTGCTCACAGTCA 	% а	2527 TGCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGGCAGGGCTGAAGCTGG 2586
& A	GTATGTGTGAAGATCCCTGGTGGGTGGCCTTCACCACGATCTTGAGCAAATTAGGAAAA	\$\$	2587 GCCTTGAAGGATGAATGTTGGATAGAAATGAGGAAGAAGACAGAGGCCTCCAAGTGA 2646
\(\frac{1}{2} \)	TGTACCCTTGGCTTGAGCGGAGTGCAGCCTTCCCCCGAGTGCATGGCTTGGAGAGCAGA	& g	2647 GAGAAGCATGAAAAATGAGCAGGGCCTGGATCAGTGGGGTGTATTCAGAGCACCTCTCC 2706
ර සි	ATCTGGGCTGCATATAAGCACACTCATCCCTTTGTTCTGGGAATCTTTGTGCAGGGCATAA	ራ 8	2707 AGATGCACCATGCATGCTCACAGTCCCTTGCCTATGTGTGGGCAGAGTGTCCCAGCCAG
i & a	CAGGCTTAGTAAGTCCAAACACAGATGACAGTGTTGTGGGTCTTGTCAGAGTTGTGG	ζο qa	2767 GIGIGCCCCCACCCCAIGICCAITIACAIGICCTICAAIGCCCACCICAAAAGGIACCTC 2826 2761 GIGICCCCCACCCAIGICCAITIACAIGICCTICAAIGCCCACCICAAAAGGIACCTC 2820
65 25	CTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTTGGAAAATGTTCTGCAGGG 	λο qq	2827 TTCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCACACTGC 2886
ç, g	TTTTC TTTTC	40	2887 TGTTTTTCCTCTTTGGTCCTTCTATCACTAAAACTCATCTTCATTCA
λο Dp		ð 8	2947 ACTAATTATTTGTTTTCCTCACTACATTGTACATGTGGGAATTACAGATAACGGAAGCC 3006 2941 ACTAATTATTTGTTTTCCTCACTACATTGTACATGTGGGAATTACAGATAAACGGAAGCC 3000
를 상 점	GCCCAGTATTCCCACTCTCCAAAGGAACTGACCAGCTTATATTTCTCAACTTCTGGGGGCCCAGTATTCCCACCTTCTGGGGGGCCCCAGTATTCCCAACATTCTGGGGGAACTGACCAGCTTATTCTCAAAAGGAACTGACCAGCTTATATTCTAAAAAGGAACTGACAGCTTATATTCTAAAAAGGAACTGACAGCTTATATTCTAAAAAAAA	Qy QD	3007 KGCTGGGGTGGTGGCTCACGCCTGTAATCCCAACACTTTGGGAGGCCAAGGCAGGC
& 8	AACTGGGTATAATCCAACCATCAAAATAGAAGACCTTGCAAGAAGCAGAGTCATTCTCCA	& g	3067 CACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGGTGAAACCCCATNTNTACTA 3126
ò	GAAGGAACTTGGGAGATGATGCGCAGATGATGAAACTGGGTTCATCCCAGTTCCAAAGA	& ଶ	3127 AAAATACGAAATTAGCCAGGTGTGGCACACATCTGTAGTCCCAG 3173

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The invention relates to a novel isolated nucleic acid and the PRO
COUNTY, antiarthritic, antirheumatic, immunosuppressive,
contiasthmatic, hepatotropic, and respiratory activity. A polymeteletic,
antiasthmatic, hepatotropic, and respiratory activity. A polymucleotide
cof the invention may have a use in gene therapy. The PRO polymetelotide
cof the invention may have a use in gene therapy. The PRO polymetelotide
cof the invention may have a use in gene therapy. The PRO polymetelotide
cof the invention may have a use in gene therapy. The PRO polymetelotide
cof the invention may have a use in gene therapy. The PRO polymetelotide
cof the invention may have a use in gene therapy. The PRO polymetelotide
cof agonist, antagonist, or antibody that appecifically binds to the
color polymeteletic content of the central core activities, osteoarthritis,
covaculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
cof thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
cof incopathic demyelinating polymeuropathy, Guillain-Barra syndrome,
cof chronic inflammatory demyelinating polymeuropathy, a hepatobiliary
cof inflammatory demyelinating polymeuropathy, a hepatobiliary
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cof inflammatory bowel disease, gluten-sensitive hepatitis, primmary
cof disease, arthem multiforme, contact dermatitis, psoriasis, an allergic
cof isease, asthma, allergic rhintis, antimumunologic disease, abullous skin
disease, asthma, allergic rhintis, antimumunologic disease, abullous contact dermatitis, poriaminatory
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cof disease, asthma, allergic rhintis, antimumunologic disease, asthma, allergic rhintis, antimumunologic disease, asthma, allergic phownonia, idiopathic pulmonary fibrosis, hypersensitivity, arti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.
                                                                                                                                                                                                                                                                                                                                                                                  ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams PM,
                                                                                                                                                                                                                                                                                                               PRO polypeptide encoding cDNA SEQ ID NO:1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1120; 2940pp; English
                                                                          BP
                                                                          ADP23942 standard; cDNA; 3299
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                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
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1021 TYGYGANCTAGGCTGCTGGANTCTCCCCTGGANACTAGGTTACACCACCATAN 1080 CTGCCACCTCTCGCGANCTCCGANCTCCTGCCCCACCTTACCCCCACCTTACCCCCACCTTACCCCCACCTTACCCCCACCTTACCCCCACCTTACCCCCC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was isolated using the method of the invention as the SCZ gene. This sequence has been previously identified as CD84, GenBank Accession No: NM 001874. CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. The proteins encoded by this sequence may be involved in the processes by which the brain responds to biological stimuli. Therefore they may provide targets, for therapeutic intervention in the treatment of schizophrenia. The SCZ sequence may be used in a new method of diagnosing susceptibility to schizophrenia in a patient. The method comprises determining the presence or absence of an allale of a linked polymorphic marker in the DNA of the patient. The polymorphic marker is present in chromosome 1422 and is linked to a gene (SCZ) having a variant form associated with a phenotype of schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTCACAGTGAATGGGATTCTGGGAGAGTCAGTCACTTTCCCTGTAAATATCCAAGAAC 186
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                                                                            schizophrenia;
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                                                                            monocyte; circulating B cell;
                                                                                SCZ; gene; CD84; platelet; monocyte; circulating allele; polymorphic marker; chromosome 1q22; ss
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                        241 GAGACTCAGAACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATAC
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Db 2401 CCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTAGAAGATGTGCATAATGTCTGC 2460 Oy 2467 TCTTGTGTAGGAGAGAAATTCCAGGACAGACAGTAAGTTAACGCTGAACTGCAGC 2526	Db 2461 TCTTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2521 2587 2581	GAGAAGCATGAAAAATGAGCAGGGCCTGGATCAGTGGGGGTGTATTCAGAGCACCTCTCC	2707 AGAIGCACCAIGCAIGCTCACAGICCCTIGCCIAIGIGGGCAGAIGICCCCAGCCAGAI	2767 2761	2827 TCCTGTAAAGCTTTCCCTGGTATCAGAATTAAAATTAATCAGGATCTTTTCACACTGC 2821 TCCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCACACTGC	2887	2941 ACTAATTATTTGCTCACTACATTGTACATGGGGAATTACAGATAAACGGAAGCC	3001 GGCTGGTGGTGGCTCACCCCTGTAACCCCAACACTTTGGGAGGCCAAGGCAGGC	3067 CACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGGTGAACC	Qy 3127 AAATACGAATTAGCCAGGTGTGGTGGCACATCTGTAGTCCCAG 31/3 	RESULT 9 ACN92105 ID ACN92105 standard; DNA; 3687 BP.	AC ACN92105; XX XX DT 02-DEC-2004 (first entry)	DE Breast cancer related marker, seq id 13255. XX XW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.	OS Homo sapiens. XX PN US2003099974-Al	03.	01;
TITIAIGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCATATGACT 	AGAGGCCTCTTGTGACTGGAGGTAACAACCCTGCCCAGTAACTGTGGGAGAGAGGGGATCA 	1441 ATAITTTGCACACCTGTAATAGCCACGCAGCCAGGCAAGGCTGTGTGTG	1501 GTATGTGTGAAGATCCCTGGTGCGTGGCCTTCACCACGCATCTTGAGCAAATTAGGAAAA 1560 1567 TGTACCTTTGGCGTGAGAGAGAGAGAGAGAGAA 1626 1567 TGTACCTTTGGCGTGAGAGAGAGAGAGAA 1626 1561 TGTACCTTTGAGAGAAAAAAAAAAAAAAA 1620	7 ATGREGATEGRATATAGE CATCOCTTEGE CONTROLLED THE CON	CAGGCTTAGTAAGTCCAAACACAGATGACAGTGCTGTGTGGGTCTCTGTCAGAGTTGTGGGCAGGCTTAGTAAGTA	1747 CTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTTGGAAAATGTTCTTTCT	1807 TCTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAGGATTTTC 1866 1801 TCTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTACAAAGCCTTATAGGATTTTC 1860	1867 TITCTGGCCAAGATTTCCTTCTGTATCACTCCAAGCAGCAGCAGCAGCAGCAGT 1926	1927 GCCCAGTATTCCCACTCTCCAAAAGGAACTGACCAGCTTATATTTCTCACACTTCTGGGG 1986 	1987 AACTGGGTATAATCCAACCATCAAAATAGAAGACCTTGCAAGAAGCAGAGTCATTCTCCA 2046 	2047 CAAGGAACTIGGGAGATGAIGCACAIGATGAACTGGGTICCATCCCAGTICCAAAGA 2106 	2107 CTCAGAGAACTAGAGTTTAAGCTGAGGCAGAGTGCCGCCACCCTGGCATGCCCCACAAAC 2166	2167 AGATCACCAGCCAGCTTACACAGGCATTAACTCTCCTCAATGAGGAAGAATCATTCACAA 2226 	2227 CTGAGCAAGACATTCATATGATCATTTAAGGAAGTGTTTCCCTTATGTGTTAGCAAGTAT 2286	2287 AATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCAATGGGCTGCAAT 2346	2347 TAGGCAGATAAAGACATCAĞTCCCAGTAAATGAATCCATAGACTCATAGCACCAACTA 2406	pagataaagacatcagtcccagtaaatgaatccatagactcatctagcaccaacta tagcactatgttaggagctgcaaggccccaaagtagaagatgtgcataatgtctgc

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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
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for breast
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                                                                                                                                                                                                                                                                                                                           Sequence 3687 BP; 1073 A; 881 C; 838 G; 874 T; 0 U; 21 Other;
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                                                                                  Novel isolated polypeptide associated with breast detecting presence of polypeptide in sample, as a
                                                                                                                                    Disclosure; SEQ ID NO 13255; 36pp; English
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DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor. Sequence 3326 BP; 959 A; 802 C; 753 G; 795 T; 0 U; 17 Other; Query Match Best Local Similarity 99.2%; Pred. No. 0; Matches 3141; Conservative 4; Mismatches 21; Indels 0; Gaps 0;	8 CASGCGTCCGTGCTTTTCCACAGAAGGTTAGACCCTCAAAGAGATGGCTCAGCACCT 67	68 AIGGAICTITGCTCCTTTGCCTGCAAACCTGGCCGGAAGCTGGAAAAGACTCAGAAAT 127	128 CTTCACAGTGAATGGGATTCTGGGAGAGTCACTTTCCCTGTAATATCCAAGAACC 187 	, 188 ACGCCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCTTATGTAACACCAGG 247	248 AGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACA 307	308 IGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGAAGACGCAGGAGA 367 	368	428 449	488 CAGCACCTGTAATGTCACACTGACATGCTCTGTAGAGAAAGAA	7. 17. r.	608 CCAAGAGCTGACTTACACGTGTACAGACCCCGGACACAATTCTGACTCCAT 6101	0 899 0 899	Qy 728 GCTGAGCGTGCTGGCTATGTTCTTCTGTTCTGTCTTCAGTGTTTTTGTT 787 nh 74.0 GCTGAGCGTGCTGTTCTTCTGTTCTGTTCTGTTCTTCAGTGTTTTTGTT 808	799 CCGTTTGTTCAAGAGAAGAAGATGCTGCCTCAAAGAAAACCATATACACATATACAT A09 CCGTTTGTTCAAGAGAAGAAGAAGAAAAAAAAACAAAATAATCAT A09 CCGTTTGTTCAAGAAGAAAAAAAAAAAAAAAAAAAAAAA	848 9. 98 0. 98	908 GGTGCTTCCCT
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The invention relates to treating a subject having a condition that benefits from modulating the balance of regulatory T cell function relative to effector T cell function, or vice versa, in a subject. The method involves administering an agent that modulates the expression or activity of a molecule selected from PTGER2 and TGFbetal, or Jagged-1, GPR-3, CBR3, CDR4, CDR9, serotonin R2C, GPR63, in stamine R-H4, GPR-8B, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-3-related kinase to the subject, such that treatment occurs. The methods are useful for diagnosing, preventing or treating conditions characterized by a too-vigorous or weak effector T cell or regulatory T cell response to antigens associated with the condition, such as in an allegic response, an autoimmune disorder, a viral infection, a microbial infection, a parasitic infection or a tumour. The present sequence represents a DNA encoding a human leukocyte differentiation CDR4 antigen, cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating a condition that benefits from modulating regulatory or effector T cell function comprises administering an agent that modulates the expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbetal, Jagged-1 or GFR-32).
                                                                                                                                                                                                                                                                                    T cell; antiallergic; immunosuppressive; virucide; antibacterial; antiparasitic; cytostatic; gene therapy; human; gene; CD83; ds; leukocyte differentiation antigen.
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                                                                                                                                                                                                                Human leukocyte differentiation antigen CD84 encoding DNA.
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09-OCT-2002; 2002US-0417343P.
18-OCT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0424481P.
AD005707 standard; DNA; 1067
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32.6%; Score 1034; DB 12; 100.0%; Pred. No. 4.4e-307; iive 0; Mismatches 0;

Length 1067;

standard; DNA; 1067

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic said sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                        cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
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Best Local Similarity 100.
Matches 1034; Conservative
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                GAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCTTA
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Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein; immune proliferative disorder; immune disorder; rheumatoid arthritis; carcinoma; autoimmune disorder; multiple sclerosis; Grave's disease; Hashimoto's disease; acquired immune deficiency syndrome; hepatotropic; osteoatthritis; allergic inflammatory disorder; viral infection; asthma; psoriasis; apoptotic disorder; systemic lupus erythematosus; bronchitis; (first Human CD84 DNA 14-NOV-2002

standard; DNA; 1040 BP

AAD43563 AAD43563

RESULT 13 AAD43563

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The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (1g) and 1g-like domains and SLMA associated protein (SAP) motifs. CD5000 DNA and protein is useful for treating disorder such as immune proliferative disorders. (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. crquired immune deficiency syndrome (AIDS)), inflammatory bowel disease (e.g. treumatord arthritis and octeoarthritis), alloratory disorders (e.g. treumatord arthritis and osteoarthritis), allorator inflammatory disorders (e.g. systemic lupus erythematosus, and psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is used in gene therapy. CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trial and pharmacogenomics), and in methods of treatment (e.g. the numan CD84 DNA used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
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diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachaxia; hepatic circulatory disorder; hepatitis; cirrhosis; acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic; immunosuppressive; neuroprotective; antiinflammatory; Crohn's disease; osteopathic; antibacterial; immunomodulator; inflammatory bowel disease; jaundice; dermatological; ulcerative colitis; AIDS; CD84; gene; ds.
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Pred. No. 6.6e-307;
); Mismatches 1;
                                                                                                                                                                                                                              "Human CD84 protein"
                                                                                                                                                                      Location/Qualifiers
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P-PSDB; AAE26238
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Human secreted protein gene 164 clone HSAWF26.

19-JAN-1999

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm. 970S-0038621P.
970S-0040161P.
970S-0040163P.
970S-0040333P.
970S-0040331P.
970S-00403312P.
970S-0043311P.
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This sequence represents a nucleic acid molecule designated Gene 164 from the human cDNA clone HSAWF26 (deposited as clone ATCC 97903 and ATCC 900499) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV5511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Fischer CL, Soppet DR, Carter KC;
P, Enderess GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
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Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAVS9511 for described uses)
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                                                                       Score 813; DB 2; I
Pred. No. 4.7e-239;
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Best Local Similarity 99.2
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Example 1; SEQ ID NO 303; 129pp; English.

The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative

disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, c.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to suburi, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional carbohydrate, vitamins, minerals, cofactors and other nutritional carbohydrate, resent sequence represents a cDNA derived from a gene concoling one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was obtained in electronic format directly from USTFO at seqdata.uspto.gov/sequence.html?DocID=6420526B1

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Best Local Similarity 99.2%;
Matches 821; Conservative

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2385 AGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTA 2445 240 121 CCCTTATGTGTTAGCAAGTATAATCGGCTAACTCCCTAAATCCCAATGAATAGTCCTAGGG TGGACAGCAATGGGCTGCAATTAGGCCAGATAAAGACATCAGTCCCAGTAAATGAATCCAT

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ALIGNMENTS

US. 09-149-476.

US. 09-149-476.

US. 09-149-476.

US. 04-15.

Sequent No. 6420526

GENERAL INVERNATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: P2002P1

CURRENT PILING DATE: 1998-09-08

EARLIER PILING DATE: 1998-03-06

EARLIER PILING DATE: 1998-03-06

EARLIER FILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

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EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                             Query Match
Best Local Similarity 100.0%;
Matches 3173; Conservative 0
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Patent No. 6812339

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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

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Sequence 1456, Application US/09949016

Sequence 1456, Application US/09949016

Patent No. 6912339

GENERAL INFORMATION:
TILL OF INVENTION: POLYMOREHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFRENCE: CLOAD1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 1456

LEAGURANT: RESEEE for Windows Version 4.0

LEAGURANT: 3296
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, ORGANISM: Human	JS-09-949-016-12299 Query Match Best Local Similarity 99.5%; Pred. No. 0; Matches 2204. Conservative 3. Mismatches 7: Indels 0: Gans 0:	AAAGCCACCACACACACACACACCTCCTGGGACTTCAAGC 101	Qy 1020 TATGAATTGTGATCTAGGCTGCTGGAATTCTCCCTCTGGAAACTGAGTTACAACC 1079	Qy 1080 ACCAATACTGGCAGGTTCCCTGGATCCTGTTCTCTGCCCAACTTTACTGGGAGATT 1139	Oy 1140 GCAAACTGCCACATCTCAGCCTGTAAGCAAAGCAGGAAACCTTCTGCTGGGGATAGCTTG 1199 Db 33327 GCAAACTGCCACATCTCAGCCTGTAAGCAAAGCAGAAACCTTCTGCTGGGCATAGCTTG 33386	Oy 1200 TGCCTAAATGGACAAATGGATGCATACCCTTCCTGAAATGACTCCCTTCTGAATGAA	1260 CAAAGCAGGTTACCTAGTATAGTTTTCCCAAACTTCTTCCCATCATAGAAAAAAAA	OY 1320 ATAATATTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCA 1379	1380 TATGACTAGAGGCCTCTTGTGACTGGAGGTAACAACCCTGCCCGGTAACTGTGGGAGAGG 14	1440 GGGATCAATATTTTGCACACCTGTAATAGGCCATGGCACACCAGCCAAGATGCTCTGCTC	1500 ACAGTCAGTATGTGTGAAGATCCCTGGTGGCGTGGCCTTCACCACGCGATTTGAGCAAATT 1500 ACAGTCAGTATGTGTGAAGATCCCTGGTGGCGTGGCCTTCACCACGCATCTTGAGCAAATT 1500 ACAGTCACTAATGTGAAGAATCCCTGGTGCGTGGCCTTCACCACGCATCTTGAGCAAATT 1500 ACAGTCACTAATGTGAAGAATCCTTGAGCATGCCTTCACCACATCTTGAGAAATT	1560 AGGARANGTOCCTTCGCTTGAGGAGATGCAGCCTTCCCCCGAGTGCAGGCTTGGATGAGATGCAGGCTTGGATGAGCATTGGATGAGCATTGGATGAGCATTGAGGAAGATGCAGGCTTGAGGAAGATGCAGCCTTTGAGGCAGAGCAGGCAG	1620 GAGCAGAATGTGGGCTGCATATAAGCACCTCATCCCTTTGTCTGGGAATCTTTGTGCAG 33807 GAGCAGAATGTGGGGTGCATATAAGCACACACCTTTGTCTGGGAATCTTTGTGGGGTGCCTTTGTGGGAATCTTTGTGGGAACGTTTGTGGGAACGTTTGTGGGAACGTTTGTGGGAATCTTTGTGGGAACGTTTGGGAACGTTTGGGAA	1680 GGCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGCTGTGTGGGTCTCTGTCAGA 11		1800 TGCAGGGTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTCAGAGCCTTATAG 18 1800 TGCAGGGTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAG 18 1800 TGCAGGGTCTAGAGACTGCTGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAG 34	1860 GATTTTCTTCTGGCCAAGATTTCCTTCTGTATCACTCAAGCAGCCTCAGCAGAA	1920 CAGCCAGGATTCCCACTCTCCAAAAGGAACTGACCAGGCTTATATTCTCACACCT

Db 33627 GGGATCAATATTTTGCACACCTGTAATA Qy 1500 ACAGTCAGTATGTGAAGATCCTGGT		Oy 1980 TCTGGGGAACTGGGTATAATCCAACCA. 2040 TTCTGGGGAACTGGGTATAATCCAACCA. 2040 TTCTCCAGAAGGAACTGGGAATGATGATGATGATGATGATGATGATGATGATGAT
OY 3060 GGCGGATCACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGGTGAAACCCCAIN 3119	RESULT 5 US-09-949-016-13198 ; Sequence 13198, Application US/09949016 ; Patent No. 6812339 ; General No. 0. 6812339 ; General No. 10012339 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF ; FILE REFERENCE: CL001307 ; CURRENT APPLICATION NUMBER: 60/241,755 ; PRIOR PILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-03 ; TABES FEATSEQ for Windows Version 4.0 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; CRANISM: Human US-09-949-016-13198	Owery Match 69.4%; Score 2202.8; DB 4; Length 37492; Best Local Similarity 99.5%; Pred. No. 0; Matches 2204; Conservative 3; Mismatches 7; Indels 0; Gaps 0; Oy 960 TTGCTGGTARAGGTGGGAAAGCAGGACAGGAAGTGAACCTCTGGGACTTCAAGC 1019 Db 33147 TCTCTGGAAGTGGGGAAAGCCACACAGGACAGAACTGATCACACCTGGGACTTCAAGC 1079 Oy 1020 TAGGAATTGGGATCTGGCGCGAATTCTCCTCTCTGCTGGAACTTCAAGC 1079 Db 33207 TATGAATTGTGATCTGGCTGAATTCTCTCTCTCTCTCTGGAAACTGATTACAACC 1079 Db 33207 TATGAAATTGTGATCTGGCTGAATTCTCTCTCTCTCTCTTGGAAACTGATTACAACC 1079 Db 33207 TATGAAATTGTGATCTTAGGTTCCTTGCTCTCTCTCTTGCTGGAAACTGATTACAACC 33266 Oy 1140 GCAAACTGGCAGGTTCCTTGAATCTTCTTCTTCTTGCTGGAAACTGATTACAACC 33366 Oy 1141 GCAAACTGCCAATTCTTAAGGAAACAAGAAAACATCTTCTTGCTGGACATTATTTTTTTT

ACABITICAGCACAGACACTACAGTTAACGCTGAA 2519 AGTCAGAAAAATACCTTATGAGGGGGCAGGGCTG 2579 AGATGCAGCCCTTCCCCCGAGTGCATGGCTTGGA 1619 ACACTCATCCTTTGTCTGGGAATCTTTGTGCAG 1679 33926 CTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAG 1859 CCAAAAGGAACTGACCAGCTTATATTTCTCACACT 1979 ATCAAAATAGAAGACCTTGCAAGAAGCAGAGTCA 2039 34346 CGAICATTTAAGGAAGTGTTTCCCTTATGTGTTAG 2279 CCCAATGAATAGTCCTAGGCTGGACAGCAATGGG 2339 MGTCCCAGTAAATGAATCCATAGACTCATCTAGCA 2399 AGCTGAGGCAGAGTGCCGCCACCCTGGCATGCCC 2159 ACAGGCATTAACTCTCCAATGAGGAAGAATCA 2219 TAGGCCATGGCACCAGCCAAGATGCTCTGCTC 33686 CACAGATGACAGTGCTGTGGGGTCTCTGTCAGA 1739

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                                                                                      34767 AAGCTGGGCCTTGAAGGATGGATGAATTTGGATAGAGAATGAGGAAGACAGAGGGCCTC 34826
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                                                                                                                                                    2640 CAAGTGAGAAGCATGAAAATGAGCAGGGGCCTGGATCAGTGGGGTGTATTCAGAGCA
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APPLICANT: Rosen et al.
TITLE OF INVORNION: 186 Human Secreted proteins;
FILE ROFINGNION: 186 Human Secreted proteins;
FILE REFRENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: E0/040,162
EARLIER FILING DATE: 1999-03-06
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,033
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
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Patent No. 6420526
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US-09-149-476-303
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,632
R FILING DATE: 1997-05-23
R PAPLICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,580 R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,314
R RILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,569
R FILING DATE: 1997-04-11
R PELLING DATE: 1997-04-11
R R FILING DATE: 1997-04-11
R R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,311
R APPLICATION NUMBER: 60/043,671 R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,583

R RFILING DATE: 1997-05-23

R RELING DATE: 1997-05-23

R RILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,618

R APPLICATION NUMBER: 60/047,618

R RILING DATE: 1997-05-23

R RILING DATE: 1997-05-23 R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,584
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,587
R FILING DATE: 1997-05-23 PILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,893
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-04-11 APPLICATION WUMBER: 60/043,674 ELING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 APPLICATION NUMBER: 60/047,592 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-04-11 FILING DATE: 1997-06-06 FILING DATE: 1997-04-11

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R APPLICATION NUMBER: 60/056,637

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,903

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,888

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,899

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,890

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,891

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R APPLICATION NUMBER: 60/056,891

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,911

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,916

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R APPLICATION NUMBER: 60/056,916
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R APPLICATION NUMBER: 60/056,892

R APPLICATION NUMBER: 60/057,761

R APPLICATION NUMBER: 60/057,761

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/047,595

R R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,588

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,585

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,586

R RAPLICATION NUMBER: 60/047,586

R RELING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

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R RILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,614

R FILING DATE: 1997-06-23

R R APPLICATION NUMBER: 60/043,578

R RILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,576

R APPLICATION NUMBER: 60/043,576

R APPLICATION NUMBER: 60/047,501

R R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/056,630
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,878
R APPLICATION NUMBER: 60/056,662
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,872
R APPLICATION NUMBER: 60/056,872
R APPLICATION NUMBER: 60/056,872
R APPLICATION NUMBER: 60/056,882
R APPLICATION NUMBER: 60/056,882
R APPLICATION DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,876
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APPLICATION NUMBER: 60/056,864
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,631
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,632
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GGCAGAGTGTCCCAGCCAGATGTGTGCCCCCACCCCATGTCCATTTACATGTCCTTCAAT 2805 2326 TGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCAT 2385 2386 AGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTA 241 AGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTA 2446 GAAGATGTGCATAATGTCTGCTCTTGTGTAGCTCAGGAGACAATTCCAGGACACAGA 301 GAAGATGTGCGCTTAGTGTTGTAGCTCAGGAGACAATTCCAGCACAGACA AGACAGAGGGCCTCCAAGTGAGAGAAGCATGAAAAATGAGCAGGGGCCTGGATCAGTGGG 2206 ATGAGGAAGAATCATTCACAACTGAGCAAGACATTCATATGATCATTAAGGAAGTGTTT 61 ATGAGGAAGAATCATTCACAACTGAGCAATCATTCATATGATCATTTAAGGAAGTGTTT 181 IGGACAGCAAIGGGCTGCAAITAGGCAGAIAAAGACATCAGTCCCAGTAAAIGAATCCAT <u> Aggagachagactanagactagacartanagaragaranan agaaranagagan agga</u> GTGTATTCAGAGCACCTCTCCAGATGCACCATGCATGCTCACAGTCCCTTGCCTATGTGT CAGTTAACGCTGAACTGCAGCTGCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATG 2566 AGGGGGCAGGGCTGAAGCTGGGCCTTGAAGGATGGATGAATTTGGATAGAAATGAGGA 1 Accerdecatrececacaaacagareaceagecagerracaeagearraacrereca 2146 ACCCTGGCATGCCCCACAAACAGATCACCAGCCTAACACAGGCATTAACTCTCCTCA Gaps ä Length 828; 1; Indels Score 813; DB 3; Pred. No. 1.1e-243; 5; Mismatches 1; EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER PEDLICATION NUMBER: 60/056,875
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER PILING DATE: 1997-08-22
EARLIER PELING DATE: 1997-06-05
EARLIER PELING DATE: 1997-06-05
EARLIER PILING DATE: 1997-06-05
EARLIER PELING DATE: 1997-06-05
EARLIER PILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/057,659
EARLIER APPLICATION NUMBER: 60/057,659
EARLIER APPLICATION NUMBER: 60/057,669
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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-06-13
EARLIER PILING DATE: 1997-06-13
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EARLIER PILING DATE: 1997-06-13
EARLIER PILING DATE: 1997-06-13 EX PELLING DATE: 1997-08-22

EX APPLICATION NUMBER: 60/056,909

EX FILING DATE: 1997-08-22

EX FILING DATE: 1997-08-22

EX FILING DATE: 1997-08-22

EX FILING DATE: 1997-08-22

EX FILING DATE: 1997-08-22

EX PILING DATE: 1997-08-22

EX APPLICATION NUMBER: 60/056,887

EX PILING DATE: 1997-08-22

EX APPLICATION NUMBER: 60/056,908

EX FILING DATE: 1997-08-22

EX FILING DATE: 1997-08-28

EX FILING DATE: 1997-08-26

EX APPLICATION NUMBER: 60/048,964

EX ELING DATE: 1997-08-06-06

EX APPLICATION NUMBER: 60/057,650

EX ELING DATE: 1997-08-05

EX FILING DATE: 1997-08-06

EX APPLICATION NUMBER: 60/057,650

EX ELING DATE: 1997-08-05

EX ELING DATE: 1997-08-05

EX ELING DATE: 1997-08-05

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EX ELING DATE: 1997-08-08-07

EX ELING DATE: 1997-08-08-07

EX ELING DATE: 1997-08-08-07

EX ELING DATE: 1997-08-08-07

EX ELING DATE: 1997-08-08-07

EX ELING DATE: 1997-Query Match 25.6%; Best Local Similarity 99.2%; Matches 821; Conservative 2686 2506 421 2626 2746 2266 셤 ò g ò 셤 ò 셤 ò 셤 g 셤 ò 셤 ઠે ð 셤 à g 8 g ઠ ò

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                                                                      GGTTCATCCCAGTTCCAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGCAGAGTGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2146 ACCCTGGCATGCCCCCACAACAGATCACCAGCCTTACACAGGCATTAACTCTCCTCA
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Pred. No. 2.8e-177,
1; Mismatches 0,
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Best Local Similarity 99.8%;
Matches 600; Conservative
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US-09-949-016-28972
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APPLICANT: VBYTER,

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARE: FREESE FORESE OF WINDOWS Version 4.0

LENGTH: 601
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                                                                  ATCAGGGATCTTTCACACTGCTGTTTTTCCTCTTTGGTCCTTCTATCACTAAAACTCA 2924
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                     GCCCACCTCAAAAGGTACCTCTTCTGTAAAGCTTTCCCT-GGTATCAGAATTA 2864
                                                                                TCTGGCCAAGATTTCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCCATGC
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Pred. No. 2.8e-177;
1; Mismatches 0;
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Patent No. 6812339
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ilarity 99.8%;
Conservative
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ses 600; Conserv
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US-09-949-016-28971/c
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; ORGANISM: Human
US-09-949-016-28971
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Sequence 28974, Application US/09949016
; Sequence 28974, Application US/09949016
; Patent No. 691239
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REFERENCE: CLO01307
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241, 755
; PRIOR APPLICATION NUMBER: 60/241, 768
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 601
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                    2203 TCAATGAGGAAGAATCATTCACAACTGAGCAAGACATTCATATGATCATTTAAGGAAGTG
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AAATTTGGATAGAGAATGAGGAAGACAGAGGGCCTCCAAGTGAGAGAAGCATGAAAATG
                                                                                    2143 GCCACCCTGGCATGCCCCACAAACAGATCACCAGCCTTACACAGGCATTAACTCTCC
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Best Local Similarity 99.8%; Pred. No. 2.8e-177;
Matches 600; Conservative 1; Mismatches 0; Indels 0;
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US-09-949-016-28974/c
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; Sequence 28973, Application US/09949016
; Patent No. 6612339
; GENERAL INFORMATION:
    TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITHER: US/09/949,016
    CURRENT APPLICATION NUMBER: US/09/949,016
    CURRENT PILING DATE: 2000-04-14
    PRIOR PILING DATE: 2000-10-03
    PRIOR PILING DATE: 2000-10-03
    PRIOR PILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SEQ ID NO 28973
    LENGTH: 601

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Pred. No. 2.8e-177;
1; Mismatches 0; Indels 0
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Best Local Similarity 99.8'
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US-09-949-016-28973/c
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; ORGANISM: Human
US-09-949-016-28973
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Sequence 49962. Application US/09949016
; Sequence 49962. Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    TITLE OF INVENTION: VOLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TURENT APPLICATION NUMBER: US/09/949,016
    CURRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR APPLICATION NUMBER: 60/237,768
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-00-03
    PRIOR FILING DATE: 2000-00-03
    PRIOR FILING DATE: 2000-00-08
; PRIOR SEQ ID NOS: 207012
; SOFTWARE: PSELSCE for Windows Version 4.0
; SEQ ID NO 49962
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241 ATGAAATTTGGATAGAGAATGAGGAAGACAGAGGGCCTCCAAGTGAGAAGAAGCATGAAAA 182
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                                                     2661 ATGAGCAGGGCCTGGATCAGTGGGGTGTATTCAGAGCACCTCTCCAGATGCACCATGCA
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Pred. No. 2.8e-177;
1; Mismatches 0;
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US-09-949-016-49962
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Best Local S
Matches 600
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US-09-949-016-28975/c

i Sequence 28975, Application US/09949016

i Batent No. 681233

i GENERAL INFORMATION:

I TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCITAND: SEC ID NOS: 207012

SOCIATARE: PEELSON WINDOWN VERSION 4.0

SEQ ID NO 28975

LENGTH: 601
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                                  ATGAGGGGGCAGGCCTGAAGCTGGGCCTTGAAGGATGAAATTTGGATAAAATGA
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CRGANISM: Human
US-09-949-016-28975
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Sequence 49964, Application US/09949016

Sequence 49964, Application US/09949016

Sequence 49964, Application US/09949016

Sequence 49964, Application US/09949016

Sequence 49964, Application:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: 18/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR PELLOR DATE: 2000-10-03

PRIOR PELLOR DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 49964

**INMAN OF 49964
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                                                                                                 2124 TAAGCTGAGGCAGAGTGCCGCCACCTGGCATGCCCCACAAACAGATCACCAGCCTT
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                                                                                                                                                    2386 AGACTCAICTAGCACCAACTACCAITAGCACTAIGITAAGGAGCTGCAAGGCCCCAAAGTA
                     241 CCCTTATGTGTTAGCAAGTATAATCGGCTAACTCCCTAAATCCCAATGAATAGTCTAAGTC
                                                                           2326 TGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAGTCCAGTAAATGAATCCAT
2266 CCCTTATGTGTTAGCAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGC
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99.8%; Pred. No. 2.8e-177.
:ive 1; Mismatches 0.
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Best Local Similarity 99.8
Matches 600; Conservative
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ORGANISM: Human
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JITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSEQ ID NO 49963

LENGTH: 601
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   CCAGTATTCCCACTCTCCAAAAGGAACTGACCAGCTTATATTTCTCACACTTCTGGGGAA 182
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                                                                                                                                      2049 AGGAACTIGGGAGAIGAIGGIGCAGAIGAIGAAACTGGGITCAICCCAGITCCAAAGACT
                                                                                                                                                                          121 AGGAACTTGGGAGATGATGGTGCAGATGAAACTGGGTTCATCCCAGTTCCAAAGACT
                                                                                                                                                                                                                                      61 CAGAGAACTAGAGTTTAAGCTGAGGCAGAGTGCCGCCACCCTGGCATGCCCCACAACAG
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Matches 600; Conservative
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Sequence 49965_Application US/09949016

Factor 49965_Application US/09949016

Fater No. 681239
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEASESEQ for Windows Version 4.0

LENGTH: 601
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                     241 GACAATTCCAGCACAGAGACACTACAGTTAACGCTGAAACTGCAGCTGCAAGTAATAGCATGA 182
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Pred. No. 2.8e-177;
1; Mismatches 0;
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Best Local Similarity 99.8
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                                                                     GGAAGACAGAGGCCTCCAAGTGAGAAGCATGAAAAATGAGCAGGGCCCTGGATCAGT
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Search completed: February 6, 2005, 00:26:49 Job time: 507 secs

Sequence 5649, Ap Sequence 6370, Ap Sequence 1579, Ap Sequence 184, App

Sequence 166284, Sequence 166284, Sequence 166286, Sequence 166286, Sequence 166286, Sequence 166286, Sequence 10, Appl. Sequence 68, Appl. Sequence 68, Appl. Sequence 68, Appl. Sequence 656, Appl. Sequence 114894, Sequence 114894, Sequence 1056, Appl. Sequence

Sequence 1056, Ap Sequence 3334, Ap Sequence 372, App Sequence 372, App Sequence 8, Appli Sequence 8, Appli

Sequence 5668, Ap Sequence 5669, Ap Sequence 5668, Ap

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DB 10; Length 3173;
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REPERENCE: P2002D9
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARR: Patentin Ver. 2.0
SEQ ID NO 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
           Query Match
99.9%; Score 3169.4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches
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CTHER INFORMATION: n equals a,t,g, or US-09-809-391-174
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LOCATION: (3119)
OTHER INFORMATION: n
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Sequence 6219, Ap
Sequence 1885, Ap
Sequence 29, Appl
Sequence 303, App
Sequence 303, App
Sequence 303, App
Sequence 303, App
Sequence 303, App
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Sequence 174, App
Sequence 174, App
                                                                                                                                                           February 5, 2005, 18:18:04; Search time 1606 Seconds (without alignments) 11371.712 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3: /cgn2 6/ptodata/2/pubpna/USO6 NEW PUB.seq:*
4: /cgn2 6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2 6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2 6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
7: /cgn2 6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
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9: /cgn2 6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2 6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-802-171-174
US-10-164-861-174
US-10-198-846-1325
US-10-723-860-6219
US-10-723-860-1885
US-10-73-860-1885
US-10-73-860-1885
US-10-73-860-1885
US-10-73-860-1885
US-10-73-860-1885
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US-09-808-171-303
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Match Length
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APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1998-03-06
APPLICATION NUMBER: 60/040,162
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,333
FILING DATE: 1997-03-07
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R APPLICATION NUMBER: 60/047,618

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,503

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,592

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,581

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,584

R FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
APPLICATION NUMBER: 60/047,615
APPLICATION NUMBER: 60/047,597
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APPLICATION WUMBER: 60/647,598
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/647,613
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APPLICATION WUMBER: 60/647,582
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,568
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APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,502
FILING DATE: 1997-05-23
                    FILING DATE: 2001-03-16
APPLICATION NUMBER: 09/149,476
FILING DATE: 1998-09-08
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/047,583
APPLICATION NUMBER: 09/809,391
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FILING DATE: 1997-03-07
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Sequence 174, Application US/09882171

Sequence 174, Application US/09882171

Publication No. US200310175858A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 186 Human Secreted proteins

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CURRENT APPLICATION NUMBER: US/09/882,171

CURRENT FILING DATE: 2001-06-18
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       Sequence 13255, Application US/10198846

Publication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Wangyao

APPLICANT: Wangyao

APPLICANT: Wangyao

APPLICANT: Wangyao

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APPLICANT: Wangyao

APPLICANT: Wangyao

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: THERAPY OF BREAST CANCER

TITLE OF INVENTION: THERAPY OF BREAST CANCER

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT FILING DATE: 2002-07-18

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13255

LENGTH: 3687
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NAME/KEY: misc_feature
LOCATION: 1, 2, 3659, 3670, 3671, 3672, 3673, 3674, 3675, 3676, 3677,
LOCATION: 3678, 3679, 3680, 3681, 3682, 3683, 3684, 3685, 3686, 3687
OTHER INFORMATION: n = A,T,C or G
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99.6%; Score 3159.8;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3158; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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Sequence 6219, Application US/10723860

| Sequence 6219, Application US/10723860
| Publication No. U320040253606A1
| GENERAL INFORMATION:
| APPLICANT: Aziz, Matasha
| APPLICANT: Zlotnik, Albert |
| TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators |
| TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators |
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US-10-723-860-1885
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publication No. U520040253606A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Albert
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2000-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR PLILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
TYPE: DNA
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Length 1067;
                          Indels
32.6%; Score 1034; DB 18;
100.0%; Pred. No. 8.8e-309;
ative 0; Mismatches 0;
  Query Match 32.6
Best Local Similarity 100.
Matches 1034; Conservative
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                                                                       CGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGTACTCACCACACCGGGTTGCTGAGC
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Pred. No. 2.3e-240;
5; Mismatches 1;
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: POZO2P2
FURRENT APPLICATION NUMBER: US/09/809,391
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or f:
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 303
LENGTH: 828
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US-09-809-391-303
IS-09-809-391-303
Publication US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
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CTHER INFORMATION: n equals a,t,g,
US-09-809-391-303
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Best Local Similarity 99.2
Matches 821; Conservative
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i Sequence 29, Application US/10436523

j Publicatation No. US2003018088A1

j GENERAL INFORMATION:

i APPLICANT: Fraser, Christopher C.

i TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

i TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

i TITLE OF INVENTION UNMER: US/10/436,523

CURRENT FILING DATE: 2003-05-12

pRIOR APPLICATION NUMBER: US/10/007,303

pRIOR APPLICATION NUMBER: US/10/007,303

pRIOR APPLICATION NUMBER: 09/706,167

pRIOR APPLICATION NUMBER: 09/706,167

pRIOR FILING DATE: 2000-11-03

i NUMBER OF SEQ ID NOS: 100

software: Patentin version 3.1

i LENGTH: 1040

i TYPE: DNA

i ORGANISM: Homo sapiens

US-10-436-523-29
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Pred. No. 1.3e-308;
0; Mismatches 1; Indels 0;
                                  1035 TAGGCTGCTGGGCT 1048
                                                                       1054 TAGGCTGCTGGGCT 1067
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Best Local Similarity 99.9%;
Matches 1034; Conservative
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R APPLICATION NUMBER: 60/043,314
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R APPLICATION NUMBER: 60/043,569
                  R APPLICATION NUMBER: 60/047,600
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                            R APPLICATION NUMBER: 60/047,617
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,618
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,503
R FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,612
R APPLICATION NUMBER: 60/047,632
R APPLICATION NUMBER: 60/047,632
R FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,674
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APPLICATION NUMBER: 60/043,313
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APPLICATION NUMBER: 60/043,315
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APPLICATION NUMBER: 60/056,886
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/043,568
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,598
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APPLICATION NUMBER: 60/047,613
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APPLICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/047,492
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,587
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| Sequence 303, Application US/09882171
| Publication No. US20030175858A1
| GENERAL INFORMATION:
| APPLICANT: Ruben et al.
| TITLE OF INVENTION: 186 Human Secreted proteins
| FILE REPRENCE: PZ00202
| CURRENT APPLICATION NUMBER: US/09/882,171
| CURRENT FILING DATE: 2001-06-18
| PRIOR APPLICATION NUMBER: 09/149,476
| PRIOR APPLICATION NUMBER: 09/149,476
| PRIOR APPLICATION NUMBER: 09/149,476
| PRIOR PILING DATE: 1998-03-08
| PRIOR PILING DATE: 1998-03-06
| PRIOR PILING DATE: 1998-03-07
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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NUMBER: 60/056,877 1997-08-22 1997-08-22 1997-08-22 1997-08-22 NUMBER: 60/056,893 1997-08-22 NUMBER: 60/056,630 1997-08-22 NUMBER: 60/056,662 1997-08-22 NUMBER: 60/056,662		23 0 0 47 58 23 0 0 0 0 47 58 23 0 0 0 0 47 58 23 0 0 0 0 0 47 59 23 0 0 0 0 0 47 59 23 0 0 0 0 0 47 50 23 0 0 0 0 47 50 0 0 0 0 47 50 0 0 0 0 0 47 50 0 0 0 0 0 47 50 0 0 0 0 0 47 50 0 0 0 0 0 47 50 0 0 0 0 0 47 50 0 0 0 0 0 47 50 0 0 0 0 0 47 50 0 0 0 0 0 47 50 0 0 0 0 0 0 47 50 0 0 0 0 0 0 47 50 0 0 0 0 0 0 47 50 0 0 0 0 0 0 47 50 0 0 0 0 0 0 47 50 0 0 0 0 0 0 47 50 0 0 0 0 0 0 0 47 50 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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2746 GGCAGAGTGTCCCAGCCAGATGTGTGCCCCCACCCCATGTCCATTTACATGTCCTTCAAT 2805 241 AGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGTC CAGTTAACGCTGAACTGCAGCTGCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATG 361 CAGTTAACGCTGAACTGCAGCTGCAAGTAATAGCAWGAACAGTCAGAAAAATACCTTATG 2566 AGGGGCCCGAGGCCTGAAGCTGAGCCTTGAAGGATGAATTTGGATAGAGAATGAGGA 421 AGGGGGCAGGGCTGGAAGCTTGAAGGATGGATGAATTTGGATAGAATGAAGGA GIGTATTCAGAGCACCTCTCCAGATGCACCATGCTCACAGTCCCTTGCCTATGTGT 541 GIGTATICAGAGCACCTYTCCAGAIGCACCAIGCATGCTCACAGICCCTIGCCTAGTGT 2146 ACCCTGGCATGCCCCACAAACAGATCACCAGCCAGCTTACACAGGCATTAACTCTCCTCA 2206 ATGAGGAAGAATCATTCACAACTGAGCAGACATTCATATGATCATTTAAGGAAGTGTTT 61 ATGAGGAATCATTCACAACTGAGCAAGACATTCATATGATGATCATTTAAGGAAGTGTTT 2326 TGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCAT 181 TGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCAT 2386 AGACTCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTA AGACAGAGGGCCTCCAAGTGAGAAGCATGAAAAATGAGCAGGGGCCTGGATCAGTGGG Gaps 1; Length 828; Indels Query Match 25.6%; Score 813; DB 10; Best Local Similarity 99.2%; Pred. No. 2.3e-240; Matches 821; Conservative 5; Mismatches 1; DR APPLICATION NUMBER: 60/056,632

OR APPLICATION NUMBER: 60/056,664

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,664

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,876

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,999

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,875

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OR APPLICATION NUMBER: 60/056,875

OR APPLICATION NUMBER: 60/056,908

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,908

OR FILING DATE: 1997-09-05

OR APPLICATION NUMBER: 60/056,908

OR FILING DATE: 1997-09-05

OR APPLICATION NUMBER: 60/056,894

OR FILING DATE: 1997-09-05

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OR FILING DATE: 1997-09-05

OR APPLICATION NUMBER: 60/056,894 2506 2626 2266 2686 PRIOR 원 장 원 임 g ò g ò g δ ፟ ద δ ò

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ACACACTCTCCAAATGGAGTGTTGGAAAATGTTCTTTCTGCAGGGTCTAGAGACTGCTGG 1821
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                                                                                                                                                                                                                                601 GGCAGAGTGTCCCAGCCAGATGTGTGCCCCCCACCCCATGTCCATTTACATGTCCTTCAAT
                                                                                                  2686 GTGTATTCAGAGCACCTCTCCAGATGCACCATGCATGCTCACAGTCCCTTGCCTATGTGT
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                                              421 AGGGGCAGGCTGAAGCTGGGCCTTGAAGGATGGATGAAATTTGGATAGAGAATGAGGA
                                                                                 2626 AGACAGAGGCCTCCAAGTGAGAAGCATGAAAAATGAGCAGGGGCCTGGATCAGTGGG
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Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 2001-07-30
PRIOR EPILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 414.2; DB 10;
Pred. No. 5.6e-117;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36774
LENGTH: 420
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Best Local Similarity 99.3%;
Matches 416; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-09-918-995-36774
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US-09-918-995-36774
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                                                                                                                                          721 ATCAGGGATCTTTTCACACTGCTGTTTTTTCCTTTGGTCCTTCTATCACTAAAACTCA 780
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661 GCCCACCTCAAAAGGYACYTCTTCTGTAAAGCTTTCCCTKGGTATCAGGAATCAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACCCTGGCATGCCCCACAACAACAGATCACCAGCCAGCTTACACAGGCATTAACTCTCCTCA
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                                                     GCCCACCTCAAAAAGGTACCTCTTCTGTAAAGCTTTCCCT-GGTATCAGGAATCAAAATTA
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                                                                                                                                                                                   Query Match 25.6%; Score 813; DB 17; Length 828; Best Local Similarity 99.2%; Pred. No. 2.3e-240; Matches 821; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                             Sequence 303, Application US/10164861
Sequence 303, Application US/10164861
SENERAL INFORMATION:
TAPLICANT: ROSEN et al.
TILE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 303
LENGTH: 928
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COTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-303
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US-10-164-861-303
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1435 AGAAGGGGATCAATATTTTGCACACCTGTAAT--AGGCCATGGCACACCAGCCAAGATGC 1492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260 CAAAGCAGGTTACCTAGTATAGTTTTCCCAAACTTCTTCCCATGATAGCACATGTAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.9%; Score 217.6; DB 9; Length 502; 92.5%; Pred. No. 5.3e-56; live 0; Mismatches 16; Indels 7;
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHEN INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LCCATION: (469)
OTHEN INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LCCATION: (473)
OTHEN INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LCCATION: (473)
NAME/KEY: misc feature
LCCATION: (483)
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Sequence 6370, Application US/10198846

Publication No. US20030099974A1

GRNERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao
                                                                                                                                                                                                                                                                                                                          COCATION: (466)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
IOCATION: (468)
                                                                                         OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (435)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (442)
LOCATION: (442)
NAME/KEY: misc feature
LOCATION: (466)
                           INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                          INFORMATION: n equals a,t,g,
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Best Local Similarity 92.5
Matches 283; Conservative
                                                NAME/KEY: misc feature LOCATION: (426)
                                                                                                                                                                              NAME/KEY: misc feature
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                                                                       LOCATION:
                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                                                                        Sequence 5649, Application US/09783590
| Patent No. US20020110850A1 |
| GENERAL INFORMATION: |
| APPLICANT: Haseltine, William A. |
| APPLICANT: Haseltine, William A. |
| APPLICANT: Li, Hacdong A. |
| APPLICANT: Rosen, Craig A. |
| APPLICANT: Rosen, Craig A. |
| APPLICANT: Rosen, Steven M. |
| TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2 |
| TITLE REFERENCE: PO-16.2C. |
| CURRENT APPLICATION NUMBER: US/09/783,590 |
| FLIE REFERENCE: PO-16.2C. |
| CURRENT APPLICATION NUMBER: 08/420,856 |
| PRIOR FILING DATE: 1994-11-21 |
| NUMBER OF SEQ ID NOS: 12485 |
| SEQ ID NO 5649 |
| LENGTH. 502
                                             1882 TCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCCATGCCCAGTATTCCCA 1940
                                                                                     302 GACACTITICITIGGAGIGCIACTICAGAAGCCITATAGGATTITICTICCTGGCCAAGATT 361
242 ACACACTCTCCAAATGGAGTGTTGGAAATGTTCTTTCTGCAGGGTCTAGAGACTGCTGG 301
                                                                                                                                                            362 TCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCCATGCCCAGTATTCCCA 420
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (370)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (468)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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LOCATION: (167)
OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (206)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (212)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (334)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,or NAME/KEY: misc feature
LOCATION: (355)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (365)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                          RESULT 12
US-09-783-590-5649
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62

1319

1377

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3108 IGAAACCCCAININIACTAAAATACGAAATTAGCCAGGTGTGGTGGCACACATCTGTAG 3167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2928 CATTCAGCCTTACAGCATAACTAATTATTTGTTTTCCTCACTACATTGTACATGTGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3048 GAGGCCAAGGCGGGATCACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2868 AGGGATCTTTTCACACTGCTGTTTTTTCCTCTTTGGTCCTTCTATCACTAAAACTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2988 TTACAGATAAACGGAAGCCKGCTGGGGTGGTGGCTCACGCCTGTAATCCCAACACTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.5%; Score 141.2; DB 15; Length 16815;
65.4%; Pred. No. 2.3e-31;
Live 3; Mismatches 103; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 184, Application US/10052482
; Beduence 184, Application US/2064A1
; Publication No. US20040072264A1
; GENERAL INFORMATION:
    APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TILLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified base

: LOCATION: (6779) .. [6878)

: OTHER INFORMATION: a, t, c, g, unknown or other

US-10-017-161-1879
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (16483)..(16615)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   CDS
(16030)..(16267)
                                                                                                                                                                                                                                                                                                                     CDS
(9933)..(9982)
                                                                                                                                                                                      CDS
(1687)..(1956)
                                                                                                                                                                                                                                                    CDS
(4564)..(4707)
                                                                                                                        CDS
(1497)..(1568)
CDS
(201)..(388)
                                                            CDS (870) .. (941)
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Best Local Similarity
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US-10-052-482-184
                                                            NAME/KEY:
LOCATION:
                                                                                                                                            LOCATION:
FEATURE:
                                                                                                                                                                                                            LOCATION:
FEATURE:
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FEATURE:
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LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 CCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGCACCACCTATGGATC 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 TTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGCTGGAAAAGACTCAGAAATCTTCACA 134
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                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 640, 642, 643, 644, 659, 668, 675, 687, 697, 725, 726, 727,
LOCATION: 728, 745, 757, 779, 781, 790, 804, 816
OTHER INFORMATION: n = A,T,C or G
               APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT PAPPLICATION NUMBER: 002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTHARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 6370
LENGTH: 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

6.7%; Score 212.4; DB 14; Length 820;
Best Local Similarity 96.7%; Pred. No. 2.9e-54;
Matches 238; Conservative 0; Mismatches 6; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1579, Application US/10017161
; Bublication No. US20030143668A1
; GENERAL INFORMATION:
    APPLICANT: SUMA, MAKIKO
; APPLICANT: ARIAMA, YUTAKA
; APPLICANT: ARIAMA, YUTAKA
; APPLICANT: ARIAMA, YUTAKA
; APPLICANT: ARIAMA, YUTAKA
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR FILING DATE: 2001-06-18
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1579
    Wang, Youzhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: source
LOCATION: (1)..(16815)
FEATURE:
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25199 GTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTCGGGAGTTTGAGA 25258
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                                                                                                                                                                                                                                                                                                                                                                                                                      3090 TTARTCTGGCCAACATGGTGAAACCCCATNTNTACTAAAAATACGAAATTAGCCAGGTGT 3149
                                                                                                                                                                   Query Match
4.4%; Score 140; DB 17; Length 96592;
Best Local Similarity 78.9%; Pred. No. 1.7e-30;
Matches 161; Conservative 3; Mismatches 40; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25319 GGTGGCAGACACCTGTAATCCCAG 25342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3150 GGTGGCACACATCTGTAGTCCCAG 3173
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 184
; LENGTH: 96592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-482-184
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Search completed: February 6, 2005, 00:53:42 Job time : 1609 secs

id95c06.x id95c06.y RC1-HT022 AGENCOURT 602915927

BP303194

BP303194

UI-HF-BM0 737641 MA

AU141507

UI-H-BIO

BY748483

wi82g07.x 502719 MA 960749 MA

AU159053

Pan trogl BY724459 DKFZp779F

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AY408981 GSS 15-DEC-2003
Homo sapiens CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarthini; Hominidae; Homo.
1 (bases 1 to 99).
1 (Alanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferritara,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,H. White,T.J., Sninsky,J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Tu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AIGGCICAGCACCACCTAIGGAICTIGCICCTITGCCTGCAAACCTGGCCGGAAGCAGCT
                                               CA425470 (CK903266 (CK903266 (CK903266 (CK903266 (CK9031154 EB1151764 (AW13969 (AW408076 (CB530813 AW141507 AW1507 AW1507 AW1507 AW15093 AW150459 EBY724459
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100.0%; Pred. No. 3.3e-210;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene trios
Science 302 (5652), 1960-1963 (2003)
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                    CK903267
BE931154
BE931154
B151764
B1151764
BY04849
AW408076
CCB530813
AM408076
CCB530813
AM41507
A1765654
BM089070
CR772231
AU159053
AG090451
BY724459
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/locus_tag="HCM3405"
                                                   CA425470
                                                                      CK903266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence
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Homo sapiens
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Matches 987; Conservative
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Best Local S
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AY408981
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AUTHORS
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JOURNAL
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602291349
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BP306350
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PM0-CT054
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                                                                                                                            5, 2005, 11:36:21; Search time 9799 Seconds (without alignments) 12325.536 Million cell updates/sec
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BP300475
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MMSP0037
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AQV16814 A
AQV10889 A
AW963140 B
BC106937 G
CV023928 1
BP3000686 B
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                     GenCore version 5.1.6
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Minimum DB Maximum DB

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Result No.

ö 110 240 3CAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 410 470 420 530 230 NCACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAAT 290 GGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGG 350 GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATC 590 9 CACCACCTATGGATCTTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGCT PACNACCTGCAAAATCTATCGTCGGCTTGGGAAACCAAAAAATTACACAGAGT **PAGAACCACGCCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTT** ACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGT Gaps 0; 30.9%; Score 979.6; DB 9; Length 987; 99.5%; Pred. No. 1.5e-208; ive 0; Mismatches 5; Indels 0 vative 421 531 ò 셤 8

AY408982

Pan troglodytes CD84 gene, VIRTUAL TRANSCRIPT, partial sequence, AY408982

RESULT 2 AY408982 LOCUS DEFINITION

ACCESSION

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us-09-882-171-174.rst

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CAGAAGCCTTATAGGATTT 1864
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                                                                                              Best Local Similarity 97.9 Matches 900; Conservative
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E. 1 (bases I to 916)

NIH-MGC http://mgc.nci.nih.gov/.

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2473 row e column: 10

High quality sequence etop: 588.
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/organism="Homo sapiens"

/organism="Homo sapiens"

/db ingle="texon 9606"

/clone="IMAGE:6281073"

/lab_host="DH10B (phage-resistant)"

/clone lib="NIH MGC 113"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:

ECORI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:
                                                                                                                                                                                                                                                                                                                            mRNA linear EST 16-JUL-2002 sapiens cDNA clone IMAGE:6281073
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GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATC
                        TTCCAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGC
                                       TTCCAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGC
                                                                        AACAATTCTGACTCCATCTCTGCCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT
                                                                                     ACTCACCACACAGGGTTGCTGAGCGTGCTTGCTATGTTCTTCTGCTTGTTCTCTGT
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AGENCOURT 8354629 NIH_MGC_113 Homo
5', mRNA Sequence.
BQ712229
BQ712229.1 GI:21851128
EST.
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AUTHORS
TITLE
JOURNAL
COMMENT
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GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

1786 1845 1426 1486 1546 1606 1666 1726 1006 1066 1186 1246 1306 719 777 300 360 420 480 629 896 9 TGCATGGCTTGGAGGAGCAGAATGTGGGCTGCATATAAGCACACTCATCCCTTTGTCTGGG GGTCTCTGTCAGAGTTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTTGG TGGGCATAGCTTGTGCCTAAATGGACAAATGGATGCATACCCTTCCTGAAATGACTCCCT 241 TGGGGATAGCTTCTGCCTAAATGGACAAATGGATGGATGCATACCCTTCCTGAAATGACTCCCT AGATGCTCTGCTCACAGTCAGTATGTGTGAAGATCCCTGGTGCGTGGCCTTCACCACGCA TCTTGAGCAAATTAGGAAAATGTACCCTTCGCTTGAGGCAGATGCAGCCCTTCCCCCGAG AATCTTTGTGCAGGCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGCTGTGT CTGAGTTACAACCACCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTC TTACTGGGAGATTGCAAACTGCCACATCTCAGCCTGTAAGCAAAGCAGGAAACCTTCTGC TCTGAATGAATGACAAAGCAGGTTACCTAGTATAGTTTTCCCAAACTTCTTCCCATCATA TCTGGAAGCTGCATATGACTAGAGGCCTCTTGTGACTGGAGGTAACAACCCTGCCCAGTA TTCCGAAGTGCAGTTTGCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTAAACCTCC TGGGACTTCAAGCTATGAAATTGTGATCTAGGCTGCTGGGCTGAATTCTCCCTCTGGAAA TTACTGGGAGATTGCAAACTGCCACATCTCAGCCTGTAAGCAAAGCAGGAAACCTTCTGC CTGAGTTACAACCACCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTC Gaps 5; Score 836.6; DB 5; Length 916; Pred. No. 1.7e-176; 0; Mismatches 14; Indels 5

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AV716814 DCB Homo sapiens CDNA clone DCBCBC06 5', mRNA sequence.
AV716814
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Xu, X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Homo sapiens cDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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/lab_host="BM25.8"
/clone_lib="DCB"
/note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
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llarity 98.3%; Pred. No. 3.1e-128;
Conservative 3; Mismatches 8;
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/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2468 row: c column: 24
High quality sequence stop: 490.
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1 (bases 1 to 890)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
CAAAAGCCTAATAGAATTT 915
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1000)
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

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High quality sequence start: 54

High quality sequence stort: 539.
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19.5%; Score 620.2; DB 5;
Best Local Similarity 95.2%; Pred. No. 5.2e-128;
Matches 692; Conservative 0; Mismatches 30;
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602291349F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4385965 5',
481 ANTTAAAGAAGTGTTTCCCCTATGTGTTAGCAAGTATAATCGGCTAACTCCTAAAATCCA 540
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis Staudt, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LiAM10068 row: b column: 14

High quality sequence stop: 638.
                                                              2310 ATGAATAGTCCTAGGCTGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAGTCC
                                                                                                               2370 CAGTAAATGAATCCATAGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TICCACAGAGAGGTIAGACCCTGAAAGAGATGGCTCAGCA - CCACCTATGGATCTTGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .1074
/organism="Homo sapiens"
/mol_type="mRNR"
/db_xref="taxon:966"
/clone="IMAGE:4385965"
                                                                                                                                                                                                                                                                                                                                                                                                  GI:12600783
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llarity 87.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2190 GCATTAACTCTCCTCAATGAGGAAGAATCATTCACAACTGAGCAAGACATTCATATGATC 2249
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                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 666)
Hegde, P., Qi,R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                          Massessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)

Contact: John Quackenbush
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fat: 301 838 3528
Fax: 301 838 0208

Email: johnq@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCCATGCCCAGTATTCCCACTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AGGAACTGACCAGCTTATATTTCTCACACTTCTGGGGAACTGGGTATAATCCAACCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AAATAGAAGACCTIGCAAGAAGAGAGAGTCATICTCCCAGAAGGAACTIGGGAGAIGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GCAGATGATGAAACTGGGTTCATCCCAGTTCCAAAGACTCAGAGAACTAGAGTTTAAGCT
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                           666 bp mRNA linear
EST375213 MAGE resequences, MAGH Homo sapiens cDNA,
AW963140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /...drailsm="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="WAGE resequences, MAGH"
/note="Vector: pBluescriptsKm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 614.4; DB 2;
Pred. No. 1e-126;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                            AW963140.1 GI:8152976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 95.2%;
Matches 633; Conservative
                                                                                                                               Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: Reverse.
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//note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse CDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
   Tel: 617 632 5180

Fax: 617 632 5180

Email: Marc_Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCAAGGGTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon.9606"
/tisuue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
Collection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 19.1%; Score 606; DB 7; Length 608; Local Similarity 100.0%; Pred. No. 7.8e-125; nes 606; Conservative 0; Mismatches 0; Indels
                                                                                                             FORWARD: ATGGCTCAGCACCAAAACTAAGCTTGAAGT
BACKWARD: TAGATCACAATTTCATAGCTTGAAGT
FINSER LENGTH: 608 Std Brror: 55.00
Plate: 11032 row: 11 column: E
Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGAAAAC
High quality sequence start: 91
High quality sequence stop: 607
POLYA=No.
Smith 858, BOSTON, MA 02115,
                                                                                                                                                                                                                                                        1. .608
/organism="Homo sapiens"
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Matches 606
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1 (bases 1 to 608)

Rual, J. F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics
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                                     262 CACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCCTTAGGTCCGA
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1499 CACAGTCAGTATGTGAAGATCCCTGGTGCGTGGCCTTCACCACGCATCTTGAGCAAAT	DD 421 CACAGICAGIANGIGAAGAICCCINGGIGGCCITCACCACGCAICTIGAGCAAAT 480 Qy 1559 TAGGAAAATGTACCCTTCGCTTGAGCAGAGCCCTTCCCCCGAGTGCAICCTTGG 1618 DD 481 TAGGAAAATGTACCCTTCGCTTGAGCAGATGCAGCCCTTCCCCCGAGTGCATGGCTTGG 540	Qy 1619 AGAGCAGAATGTGGG-CTGCATATAAGCACACTCATCCCTTTGTGGGAATCTTTG 1674	RESULT 11 BP303350 LOCUS BP303350 BP303350 DEFINITION BP303350 Sugano cDNA library, macrophage Homo sapiens cDNA clone	ACCESSION BP303350 VERSION BP303350.1 GI:52232310 VERSION BP303350.1 GI:52232310 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Butheria; Primates; Catarrhini; Hominidae; CE 1 (bases 1 to 582) RS Suzuki,Y., Yamaahita,R., Shirota,M., Sakakibara,Y., C Mizushima-Sugano,J., Nakai,K. and Sugano,S.	TITLE Sequence comparison or numan and mouse genes reveals a nomologous block structure in the promoter regions JOURNAL Genome Res. 14 (9), 1711-1718 (2004) COMMENT CONTACT: Yutaka Sizuki	cie lina oky ifi	/organism="Momo saplens" /mol_type="mRNA" /db_xref="taxon:9606"	/clone="MpE08190" /cell_type="macrophage" /clone_lib="Sugano cDNA library, macrophage"	Okligh Watch 18.3%; Score 582; DB 5; Length 582; Cane 18.3%; Pred. No. 1.9e-119; Matche 582; Oheographive 0. Gane 0.	204 ATTGCTTGGACTTCTAAAACATCTGTTGTTAATGTAACACCAGGAGACTCAGAAACAGCA 263 1 ATTGCTTTGAACTTCTAAAACATCTGTTGTTATGTAACACCAGGAGACTCAGAAACAGCA 263	264 CCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCTTAGGTCCGAAC	324 TACAATCTGGTCATTAGCGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	384 AATACACAGGCTGATCCTACACCACCACCACCACCACACACA	444 CITGGGAAACCAAAAATTACACAGAGTTTAATGGCATCTGGAACAGCACCTGTAATGTC	241 CIIGGGAAACCAGAAATAACAGGAIITAAIGGCAICIGIGAACAGAAGAACAGAAC
OY 591 TICCAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGC 650	Qy 651 AACAAT 656 Db 601 AACAAT 606	RESULT 10 BP300686 LOCUS BP300686 598 bp mRNA linear EST 17-SEP-2004 DEFINITION BP300686 Sugano cDNA library, macrophage Homo sapiens cDNA clone	ACCESSION MP801128, mRNA sequence. ACCESSION BP300686.1 GI:52229646 KEYWORDS EST. SOURCE Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REPERENCE 1 (bases 1 to 598) AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S. TITLE Sequence comparison of human and mouse genes reveals a homologous	block structure in the promoter regions JOURNAL Genome Res 14 (9), 1711-1718 (2004) COMMENT Contact: Yutaka Suzuki Department of Virology	Instructe or Medical Science, University or Tokyo 4-6-1, Shirokanedata. Minatoku, Tokyo 108-8639, Japan Email: ysuzukidaims.u.tokyo.ac.jp. FEATURES Location/Qualifiers	/ 0.59e / Organiem="Homo sapiens" /mol_type="mRNA" /Ab_xref="taxon:9606" /clone="MPE01728" /cell_type="macrophage"	/clone_lib="Sugano cDNA library, macrophage"	Query Match 18.4%; Score 585; DB 5; Length 598; Best Local Similarity 99.8%; Pred. No. 4e-120; Matches 596; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	Oy 1079 CACCAATACTGGCAGGTTCCCTGGATCCTGCTCTGCCCAACTCTTACTGGGAGAT 1138	OY 1139 TGCAAACTGCCACATCTCAGCCTGTAAGGAAAGCAGGAAACCTTCTGCTGGTGGCATAGCTT 1198 	Qy 1199 GTGCCTAAATGGACAAATGGATGCATACCCTTCCTGAAATGACTCCCTTCTGAATGAA	OY 1259 ACAAAGCAGGTTACCTAGTATAGTTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAA 1318 	Qy 1319 AATAATTTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGC 1378 	Qy 1379 ATATGACTAGAGGCCTCTTGTGACTGGAGGTAACAACCCTGCCCAGTAACTGTGGGAGAA 1438	Qy 1439 GGGGATCAATATTTGCACACCTGTAATAGGCCATGGCACACCAGCCAAGATGCTCTGCT 1498 16

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590 bp mRNA linear EST 09-SEP-2002
UI-FF-BNO-aen-f-02-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone
IMAGE:3064850 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapber@mail.nih.gov
Email: cgapber@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
Clone distribution: MGC clone distribution informatio
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M.3 Forward.
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Best Local Similarity 99.1%; Pred. No. 8.7e-119;
Matches 582; Conservative 0; Mismatches 5; Indels
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/clone="IMAGE:3064850"
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Mosapiens (human)

Mosapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 580)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mitshima-Sugano,J., Nakai,K. and Sugano,S.

Squence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)

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1nstitute of Medical Science, University of Tokyo
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Email: ysuzuki@ims.u-tokyo.ac.jp.
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                                                 564 GGAGAAGAGGTAATGTCCTTCAAATCTTCCAGACTCCTGAGGACCAAGAGCTGACTTAC
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/clone_lib="Sugano cDNA library, macrophage"
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ive 0; Mismatches 0; Indels
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/mol_type="mRNA"
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                    Length 581;
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                Score 577.8; DB 5;
Pred. No. 1.6e-118;
0; Mismatches 2;
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/mol_type="mRNA"
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99.7%;
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Best Local Similarity 99.7
Matches 579; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,R. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
AL Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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BP299453 Sugano cDNA library, macrophage Homo sapiens cDNA clone MPC08221, mRNA sequence.
GCCAAGATTTCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCCATGCCCAG 1932
                                                                                                                                       TATTCCCACTCTCCAAAAGGAACTGACCAGCTTATATTTCTCACACTTCTGGGGAACTGG 1992
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                  GAGGGTGGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAGGATTTTCTTCTTG
                                                                                         GCCAAGATTTCCTTCTTTATATCACTCCAAGCAGCCTCCAGGAGAAGAAGAAGCAGCCATGCCCAG
                                                                                                                                                           124 TATTCCCACTCTCCAAAAGGAACTGACCAGCTTATATTTCTCACCACTTCTGGGGAACTGG
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301 GAGCAGAATGTGGGCTGCATATAAGCACACTCATCCTTTGTCTGGGAATCTTTGTGGGG 360
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                                                                                                                                              120
                                                                                                                           0; Gaps
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